

STIC-Biotech/ChemLib

152404

mg

From: Kaushal, Sumesh
Sent: Tuesday, May 03, 2005 5:45 PM
To: STIC-Biotech/ChemLib
Subject: 10657852: SEQ search

10657852: SEQ search

Please search

- **SEQ ID NO:3**
- **SEQ ID NO:15**

S. Kaushal

AU1636, REM2.B85
Ph: 571-27-20769
Mail Box: REM2.C70

RECEIVED
MAY - 4 2005
STIC-Biotech Division
(STIC)

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: *5/6/05*
Date Completed: *5/11/05*
Searcher Prep/Rev. Time: _____
Online Time: _____

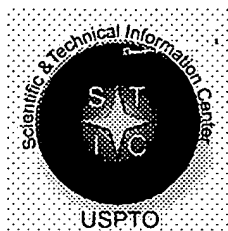
Type of Search

NA#: *1* AA#: *1*
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: *out*
WWW/Internet: _____
Other(Specify): _____

This Page Blank (uspto)



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 152404

TO: Sumesh Kaushal
Location: rem/2b85/2c70
Art Unit: 1636
Wednesday, May 11, 2005

Case Serial Number: 10/657852

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Kaushal,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

QM protein - protein search, using sw model

Run on: May 9, 2005, 20:12:52 ; Search time 65 Seconds
(without alignments)
2103.464 Million cell updates/sec

Title: US-10-657-852A-15
Perfect score: 1385
Sequence: 1 MPYMAKCCMLLVFLGLFILO.....NTVSGSNHIVSGSNKVVTDG 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	530	38.3	118	2 Q9M3W4	Q9m3w4 lolium pere
2	262	18.9	1010	2 Q8H3W8	Q8h3w8 oryza sativ
3	258.5	18.7	1036	2 Q9FN37	Q9fn37 arabidopsis
4	221.5	16.0	1124	2 Q63UH1	Q63uh1 burkholderi
5	218	15.7	1012	2 Q62KN5	Q62kn5 burkholderi
6	212	15.3	353	2 Q9ZNX4	Q9znx4 petunia hyb
7	204	14.7	1021	1 PSKR DAUCA	Q8lbp4 daucus caro
8	201	14.5	1065	2 Q66QA4	Q66qa4 oryza sativ
9	199.5	14.4	784	2 Q9C9H6	Q9c9h6 arabidopsis
10	197.5	14.3	751	2 Q94DW7	Q94dw7 arabidopsis
11	197.5	14.3	751	2 Q9FGQ5	Q9fgq5 arabidopsis
12	196	14.2	1102	2 Q69KC3	Q69kc3 oryza sativ
13	195.5	14.1	1023	2 Q84NG8	Q84ng8 hordeum vul
14	194	14.0	622	2 Q66CJ0	Q66cj0 yersinia ps
15	194	14.0	917	2 Q75GM9	Q75gm9 oryza sativ
16	194	14.0	1063	2 Q67IT7	Q67it7 oryza sativ
17	193.5	14.0	372	2 Q89J37	Q89j37 bradyrhizob
18	192.5	13.9	846	2 Q9C9H7	Q9c9h7 arabidopsis
19	192	13.9	727	2 Q67TW5	Q67tw5 oryza sativ
20	192	13.9	1060	2 Q6ZGM3	Q6zgm3 oryza sativ
21	190.5	13.8	943	2 Q9SRL7	Q9srl7 arabidopsis
22	190.5	13.8	1008	1 PSKR ARATH	Q9zvr7 arabidopsis
23	190	13.7	622	2 Q8ZGB5	Q8zgb5 yersinia pe
24	189.5	13.7	605	2 Q6K9D3	Q6k9d3 oryza sativ
25	188.5	13.6	922	2 Q9L964	Q9l964 moraxella c
26	188.5	13.6	1011	2 Q6ZOA9	Q6zoa9 oryza sativ
27	187.5	13.5	784	2 Q9LS79	Q9ls79 arabidopsis
28	186.5	13.5	465	2 Q8I4Z3	Q8i4z3 plasmodium
29	186	13.4	641	2 Q9LDG0	Q9ldg0 oryza sativ
30	186	13.4	645	2 Q9SVN1	Q9svn1 arabidopsis
31	185	13.4	1012	2 Q7XP13	Q7xp13 oryza sativ

32 184.5 13.3 836 2 Q9SCT4 Q9sct4 arabidopsis
33 183.5 13.2 380 2 Q6Z3T9 Q6z3t9 oryza sativ
34 183.5 13.2 1051 2 Q67IT2 Q67it2 oryza sativ
35 182 13.1 941 2 Q9XD54 Q9xd54 moraxella c
36 181.5 13.1 718 2 Q6ET59 Q6et59 oryza sativ
37 181 13.1 653 2 Q8LKV9 Q8lkv9 aegilops ta
38 181 13.1 883 2 Q9M9X1 Q9m9x1 arabidopsis
39 181 13.1 1065 2 Q9LG15 Q9lg15 oryza sativ
40 180.5 13.0 703 2 Q6R2J8 Q6r2j8 arabidopsis
41 180 13.0 998 2 Q8LJI9 Q8lji9 oryza sativ
42 180 13.0 1047 2 Q6K213 Q6k213 oryza sativ
43 180 13.0 1080 2 Q69P46 Q69p46 oryza sativ
44 179.5 13.0 983 2 Q8L7L6 Q8l7l6 arabidopsis
45 179.5 13.0 983 2 Q9ZUK3 Q9zuk3 arabidopsis

ALIGNMENTS

RESULT 1
Q9M3W4 PRELIMINARY; PRT; 118 AA.
ID Q9M3W4
AC Q9M3W4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ice recrystallisation inhibition protein (Fragment).
OS Lolium perenne (Perennial ryegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poae; Lolium.
OX NCBI_TaxID=4522;
RN [1]
RP SEQUENCE FROM N.A.
RA Sidebottom C.M.;
RL Thesis (1999), University of York.
RN [2]
RP SEQUENCE FROM N.A.
RA Sidebottom C.M.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277399; CAB87814.1; -
DR PDB; 1I3B; Model; A=1-118.
FT NON_TER 1
FT CHAIN <1 118
SQ SEQUENCE 118 AA; 11766 MW; 0362C1B4F98AE9F8 CRC64;
Query Match 38.3%; Score 530; DB 2; Length 118;
Best Local Similarity 85.5%; Pred. No. 3.5e-32;
Matches 100; Conservative 10; Mismatches 7; Indels 0; Gaps 0;
QY 150 DEEPNTISGTTNSVSGSNVSGNDNTVTVSGNNHVSNNNTVTVSGNDNTVTVSGNNHVS 209
Db 1 DQQNTISSNNTVTRSGKNVAGNDNTVSGDNNVSGSNNTVTVSGNDNTVTVSGNNHVS 60
QY 210 GTKGHIVTDNNNVSGNDNNVSGSFHTVSGEHTVSGNNHVSNNHVSNNHVSNNHVS 266
Db 61 GTNHIVTDNNNVSGNDNNVSGSFHTVSGHNTVSGNNHVSNNHVSNNHVSNNHVS 117
RESULT 2
Q8H3W8 PRELIMINARY; PRT; 1010 AA.
ID Q8H3W8
AC Q8H3W8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Putative phytoosulfofokine receptor.
GN Name=P0585H1.109;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;


```
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Putative outer membrane protein.
GN ORFNames=BPSL1631;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
RA Feitwell T., Fraser A., Hance Z., Hauser H., Hoiroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA Whitehead S., Yeate C., Barrell B.G., Oyston P.C.F., Parkhill J.,
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
DR EMBL; BX571965; CAH35630.1; -.
SQ SEQUENCE 1124 AA; 104844 MW; 90EC4527E9017602 CRC64;

Query Match 16.0%; Score 221.5; DB 2; Length 1124;
Best Local Similarity 27.7%; Pred. No. 6.6e-08;
Matches 74; Conservative 41; Mismatches 99; Indels 53; Gaps 9;

QY 36 ALRGLAENLSGKGAVALRAAWSCASCCSWEGVCETASGRVVALRPKR-----GLGGI 89
DB 316 SLTGADNVLSL-----TSLSTVNANLAGLQTSVDNVVSYDDPKSAITLGGAGVT 367
QY 90 IPSSIGELDHLRYLDLSGNSLVEGPKSLQ-----IRLKSLLTDSQSLGMSIN 138
DB 368 TPVLLTNVAAGKIAATSTDAVNGSQLYTLQBFPSQQYDILLTSQVSSLTSVSGI-QGSVS 426
QY 139 MLLHVSRRRLDEPNTISGTN-----NSVSGSGNNVSGNDNTVVGSGNNHVSNNVT 192
DB 427 -----ANTGTASGDNSTASGDNATASGTNTANGTNTASG-DNSTASGTNASASGENST 480
QY 193 VVTGSDNTVVGSG-----NHVVGPKHIVTDNNVVGSGNDNNVSGSFEHTVGS 238
DB 481 -ATGDTASGSGNSTANGTNTASGDNSTASGTNASATGENSTATGTDSTASGNSSTANG 539
QY 239 EHNVTSGSGNNVSGSNHIVSGSNKVT 265
DB 540 TNSTASGDNSTASGTNASASGENSTAT 566

RESULT 5
Q62KN5 PRELIMINARY; PRT; 1012 AA.
AC Q62KN5;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Outer membrane protein, putative.
GN ORFNames=BMA1027;
OS Burkholderia mallei ATCC 23344.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=243160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 23344;
RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
RA Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
```

```
RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.P., Madupu R.,
RA Mohammad Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
RA Selenigut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
RA Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251 (2004).
DR EMBL; CP000010; AAU48866.1; -.
SQ SEQUENCE 1012 AA; 94758 MW; 53C27D16C62FBBDE CRC64;

Query Match 15.7%; Score 218; DB 2; Length 1012;
Best Local Similarity 30.9%; Pred. No. 1.1e-07;
Matches 55; Conservative 31; Mismatches 72; Indels 20; Gaps 4;

QY 106 SGNLSLVEGPKSLQIRLKSLLTDSQSLGMSINMLLHVSRRRLDEPNTISGTN----- 160
DB 545 SSGDSSTASGTNASATGENSTATGTDSTASGNSSTANGTNS--TASGDNSTASGTNASATG 602
QY 161 -NSVSGSGNNVSGND-----NTVVGSGNNHVSNGSN-----NTVVTGSDNTVVGSGNHV 207
DB 603 ENSTATGTDSTASGNSSTANGTNTASGDNSTASGTNASATGENSTATGTDSTASGNSST 662
QY 208 VSGTKHIVTDNNVVGSGNDNNVVGSGSFHTVSGEHTVVGSGNNHIVSGSNKVT 265
DB 663 ANGANSTASGNSSTANGTNTASGNSSTANGTNTASGNSSTANGTNTASGTNASATGENSTAT 720

RESULT 6
Q9ZNX4 PRELIMINARY; PRT; 353 AA.
AC Q9ZNX4;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE PGPS/D4 precursor (LRR protein S/D4).
GN Name=PGPS/D4;
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Germinating petunia pollen treated with kaempferol;
RX MEDLINE=2031712; PubMed=10859200; DOI=10.1104/pp.123.2.699;
RA Guyon V.N., Astwood J.D., Garner E.C., Dunker A.K., Taylor L.P.;
RT "Isolation and characterization of cDNAs expressed in the early stages
RT of flavonol-induced pollen germination in petunia.";
RL Plant Physiol. 123:699-710 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Germinating petunia pollen treated with kaempferol;
RA Guyon V., Astwood J.D., Taylor L.P.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Guyon V.N., Astwood J.D., Garner E.C., Dunker A.K., Taylor L.P.;
RT "Isolation and characterization of cDNAs expressed in the early stages
RT of flavonol-induced pollen germination in petunia.";
RL Life Sci. Adv. Plant Physiol. 123:699-710 (2000).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=15272880; DOI=10.1111/j.1365-313X.2004.02162.x;
RA Guyon V., Tang W.H., Monti M.M., Raiola A., Lorenzo G.D.,
RA McCormick S., Taylor L.P.;
RT "Antisense phenotypes reveal a role for SHY, a pollen-specific
RT leucine-rich repeat protein, in pollen tube growth.";
RL Plant J. 39:643-654 (2004).
DR EMBL; AF049920; AAD02546.2; -.
DR EMBL; AF325673; AAK11220.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR Pfam; PF00560; LRR 1; 8.
DR PRINTS; PR00019; LEURICHRPT.
```



```
Query Match 14.7%; Score 204; DB 1; Length 1021;
Best Local Similarity 24.6%; Pred. No. 1.2e-06;
Matches 81; Conservative 56; Mismatches 94; Indels 98; Gaps 14;

QY 10 MLLVFLGPILO--VAGATWSCHHDDHAL-----RGLAENLSGKGAVALRAAWS-----57
DB 8 VILLVGFVQIVVNSQNTNSNDLKALEGFMRLGLESSIDG-----WKWNSS 58
QY 58 -GASCCSWEVGCETA-----SGRVVALRLPKRGIGGIIPSGISGELDLRLVLDLS 106
DB 59 FSNCCDWGISCKSSVSLGLDDWESGRVVELELGRKLSGKLSVAKLDQLKVLNT 118
QY 107 GNSLVGEVPSKL-----QIRLSKSTTDSQSLGMSINMLHVSSRRRLDEEPTISG----158
DB 119 HNSLSGSIASLNLNLEVLDSNDFS---GLTFPSLINLPSLRVLNVVENSFHGLIPA 175
QY 159 --TNN-----SVGSGSNVNVSGNDNTV--VSGNNHVS-----SNTTV 194
DB 176 SLCNLPRIREDIAMNYPDGSIPVGTGNCSSVEYLGASNNLSGSIPOELFQLSNLVL 235
QY 195 TGSNDTVVSGNHVSGTKHIVTNNNVVSGNDNNVSGSFHV-----SGEHNTVS 244
DB 236 ALQNNLSGA-----LSKLGKLNGLDLSNKNFSKIPDVLELNKLVYFSAQSNLFN 291
QY 245 GS-----NNTVSGSNHI 256
DB 292 GEMPSLSNSRSISLLSRNNTLSGGIYL 320

RESULT 8
Q66QA4 PRELIMINARY; PRT; 1065 AA.
ID Q66QA4
AC Q66QA4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Putative leucine-rich repeat receptor-like kinase.
OS Oryza sativa (indica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39946;
RN [1]
RA He G.M., Li K.G., Yang J.S.;
RP "Oryza sativa (indica cultivar-group) chromosome 2 genomic sequence.";
RT Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RA He G.M., Li K.G., Yang J.S.;
RP "Isolation and expression pattern of putative LRR (leucine-rich
RT repeat) receptor-like kinase in rice.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY730046; AAU12611.1;
DR EMBL; AY714494; AAU12603.1;
DR GO; GO:0016301; F-kinase activity; IEA.
DR GO; GO:0004872; F-receptor activity; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR011611; LRR.
DR InterPro; IPR003885; LRR_cyst.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR003591; LRR_tyr.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00560; LRR_1; 20.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR PDom; PD000001; Prot_kinase; 1.
DR SMART; SM00365; LRR_SD22; 6.

DR SMART; SM00369; LRR_TYP; 8.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TYK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; Receptor.
SQ SEQUENCE 1065 AA; 116827 MW; CFE570663C05BFOA CRC64;

Query Match 14.5%; Score 201; DB 2; Length 1065;
Best Local Similarity 24.6%; Pred. No. 2.1e-06;
Matches 87; Conservative 54; Mismatches 98; Indels 114; Gaps 16;

QY 7 KCMLVFLVFGF-----ILOVAGATWSCHHDDHALRGLAENLSGKGAVALRAAA 55
DB 12 KCSNRCFDIFLRFNLAFAALLLLLSLASPTS-SCTEQERSLLQLFLSSLSDDGLAV-SW 69
QY 56 WSGASCCSWEVGCETAASGRVVALRLPKRGIGGIIPSSIGELDLRLVLDLSGSLVCEVP 115
DB 70 WNAADCCKWEGVTC-SADGTVTVDVSLASKGLEGRISPSLGNLTGLRLRLNLSHNSLSGGLP 128
QY 116 KSLQIRLKSLLTDSQSLGMSINML-----LHVSSRRRLDEEPTNT-- 155
DB 129 -----LELMASSTIVLDISFNLLKEETHELPSSTPARPLOVINISSNLTQGFPSATW 182
QY 156 -----ISGTNNS-VSGSGSNVNVSGNDN-TVSGNNHVS-----NNTVVTG 196
DB 183 EMMKNLVMLNASNNSPTGOIPSNFCSRPSLTVALCYNHLNGSIPPFGNCLKLRVLKA 242
QY 197 SDNTVVS-----NHVVSQT-----KHIVT-----DNNV----- 221
DB 243 GHNNLSGNLPGLDFNATSLLEYLFPNNELNGVINGTLIVNRLNLTDLDEGNNINGRID 302
QY 222 -----VSGNDNNVSGSF-----H--TVSGEHTVSGSNNTVSGSN 254
DB 303 SIGQLKRLQLDLHGDNNISGELPSALSNCNTHLITINLKNFNSGNLSNVNFSN 355

RESULT 9
Q9C9H6 PRELIMINARY; PRT; 784 AA.
ID Q9C9H6
AC Q9C9H6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Putative disease resistance protein; 69620-67266.
GN Name-P28A9.23;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopses.
OX NCBI_TaxID=3702;
RN [1]
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RA Town C.D., Kaul S.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC016163; AAG51813.1;
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR Pfam; PF00560; LRR_1; 20.
DR PRINTS; PR00019; LEURICHRPT.
DR SQ SEQUENCE 784 AA; 88730 MW; 8770246421192623 CRC64;

Query Match 14.4%; Score 199.5; DB 2; Length 784;
Best Local Similarity 24.2%; Pred. No. 1.9e-06;
Matches 80; Conservative 51; Mismatches 80; Indels 119; Gaps 15;
```


Db 251 MSNNLSGEVPKSLFNTSSLTALFLOQNSFVGSPAIAMSSPI----KYISLRDNCISGT 306

22

DD 307 IFESDGHKIEIEIIMSVNNLSGDUVFFSFTFNISSELIFFET'IGNNSTV 332

RESULT 13

Q84NG8

ID Q84NG8 PRELIMINARY; PRI; 1023 AA.
AC Q84NG8:

DT 01-JUN-2003 (TREMBLrel. 2

DT	01-MAR-2004 (TREMBlrel. 26. Last annotation update)
DI	01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DE Putative receptor kinase.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; M

NCBI_TaxID=4513;
OX

RN [1]
PP SEQUENCE FROM N A

RX PubMed=14663527; DOI=10.1139/g03-071;

RA GU Y.Q., ANDERSON O.D., LONDELE C.F., KONG X., CHIBBAR K.N.,
RA IJAZO G.R.:

RT "Structura

RL Genome 46:1084-1097 (2003).

CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/thr

DR GO; GO:0016740; F:transferase activity; IEA.

DR GU; GO:0006468; F:protein amino acid phosphorylation; IEA:
DR InterPro: IPR011009; Kinase like.

DR InterPro; IPR001611; LRR.

DK InterPro; IPR000050; Eukaryotic
DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR PRINTS; PR00019; LEURICHRPT.

DR PRODOM; PD000001; PROT_KINASE; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSTIE; PS00108; PROTEIN_KINASE_S1; I.
KW ATP-binding: Kinase: Receptor: Serine/threonine-protein kinase:

KW Transfere.

SEQUENCE 1023 AA; 110107 MW; 05EB02D3C411171C0 CRC047;

Query Match	14.1%;	Score 195.5;	DB 2;	Length 1023;
	20.0%	Score 195.5	DB 2	Length 1023

Best local similarity	30:30; 120:120	30:30; 120:30	30:30; 30:30						
Matches	84;	Conservative	37;	Mismatches	113;	Indels	43;	Gaps	13;

2 DEYMA KCCMI I VEI CETI QINCATSWSCHDDI HAI PGI AENI SCKCAVPI PAAW-----S 57

[illegible]

UP 5 PWLRLIAL'I'I'IALLEHPSITSSSVSTAH-DLPALLEF-NSLTINDPLGALSSWINGS 62

QY 58 GASCCSWEGVCETA-SGRVVALR LPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPK 11

db 63 THGFCSWTGVECCSAHPGHVKALRLOGGLSGTISPFLGNLSRLRALDLSGNKLOGQIPS 12

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

[illegible]

Db 123 SIGNCFALRTLNLNSVNSLSGAIPFAMGNLSKLL-----VLSVSRNDISGTIPTSFAGLA I 17

Qy 169 NVVSGNDNTVVSGNNNHVSG-----SNNTVVTG---SDNTVVGSNHVVSGTKHIVTDNN 21

177 TV-----AVESVARNHVHGOVPPWI.GNI.TALEDI.NMADN--TMSGHVPPALSKLINLRS 22

QY 220 NVSGNDNVSGSFHIVSGHNIVSGSN ---NIVSGS 253

```
Db 229 LTVA--INNLOGLIPVLFNMSLSLECLNFGSNQLSGS 263
RESULT 14
Q66CJ0 PRELIMINARY; PRT; 622 AA.
AC Q66CJ0;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Putative exported protein precursor.
GN ORFNames=YPTB1413;
OS Yersinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=273123;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=IP 32953;
RX PubMed=15358858;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hinebusch B.J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RA "Insights into the genome evolution of Yersinia pestis through whole
RT genome comparison with Yersinia pseudotuberculosis."
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
RW EMBL; BX936398; CAH20653.1; -.
KW Signal.
FT SIGNAL 1 32 Potential.
SQ SEQUENCE 622 AA; 65230 MW; 30B8C7D77A3D73CD CRC64;
Query Match 14.0%; Score 194; DB 2; Length 622;
Best Local Similarity 26.8%; Pred. No. 3.6e-06;
Matches 68; Conservative 48; Mismatches 78; Indels 60; Gaps 12;
Qy 43 NLSGKGVRLRAAAGSCCSWEGVGCETASGRVVALPKRGGLGIPPSIGELHLRY 102
Db 41 NNGNGTINIFASGNNDIHTLTGLNEL-----LGGF-----SNHL-- 77
Qy 103 LDLSGNSLVGVPKSLQIRLKSLLTDSQSLQMG-----SINMLHVSRR-L 149
Db 78 IDSHNNTINGQSNNL-VSSDGTISALSGLGLFYGAQNNTLNSNNLLIVTQGSTII 136
Qy 150 DEEPTNTSGTWNVSGSGNNVSGNDNTVVS-----GNNHVSNNVTVTGSD 198
Db 137 DSDSNTVSGISNNLTIESNII-GNENSCYSDPASPGAWCVDNQNTLIGSDNNTITGAL 195
Qy 199 NTVVGSNH--VVSCTKHIVTDNNVSGNDNNVSGSPHTVS-GEHNTVSGNNVTGSGN 254
Db 196 NGLHNSHNDIIASVNNIMDTHNNIAG-----GHYNTISGGNNDIFGSENNVTDST 249
Qy 255 HI-VSGSNKVVTDG 267
Db 250 DANINGSNNYVIDG 263
RESULT 15
Q75GM9 PRELIMINARY; PRT; 917 AA.
AC Q75GM9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein OSJNBa0018K15.10.
GN Name=OSJNBa0018K15.10;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
SEQUENCE FROM N.A.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Lee P.-F., Chang S.-J., Chen H.-C., Chen S.-K.,
RA Chen T.-R., Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y.,
RA Hsiao S.-H., Hsiung J.-N., Hsu C.-H., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RA Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC144737; AAT01367.1; -.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR003591; LRR typ.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR02290; Ser Thr kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00560; LRR_1; 14.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00369; LRR_TYP; 5.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Ty-Kc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
KW ATP-binding; Hypothetical protein.
SQ SEQUENCE 917 AA; 96507 MW; AE6DC9F7DD6E0B77 CRC64;
Query Match 14.0%; Score 194; DB 2; Length 917;
Best Local Similarity 26.3%; Pred. No. 5.9e-06;
Matches 81; Conservative 43; Mismatches 108; Indels 76; Gaps 12;
Qy 6 AKCCMLLVFLGFIILQVAGATSWSCHDDHLHALRGLAENLSKGAVRLRAAWS--GASCCS 63
Db 4 ATAALLLLTLAAILAAAGAV-----NDVLALVVKSGVSDPGGV--LAAWSEADRA 56
Qy 64 WEGVGCETASGRVVALPKRGGLGIP-SSIGELHLRYLDLGSNLVGEVPSKQLRL 122
Db 57 WPGVSCDARAGVDAVALPSAGLSGRLPSALLRLDALLSLALPGNNLSGLPDALPPRA 116
Qy 123 KSLTTDSQSL-----GMGSINM-----LLHVSRRRTIDEEPNTISG 158
Db 117 RALDLSANSLSGYLPALALSCGSLVSNLSGNLLSGVPDGIWLSPLSLRSLDLGSNQLAG 176
Qy 159 TNNVSGSG-----SNNVSGNDNTVVS-----GNNHVSNNVT--V 194
Db 177 ---SVPGGFPRSSSLRVLDSLRLLEGEIPADVGEAGLKLSDVGHNLFTGELPESLRL 233
Qy 195 TGSNTVVGNNHV-----VSGTKHIVTDNNVSGNDNNVSGSFHTVSGEHTVVS 244
Db 234 TGLSLGAGGNALAGELPGWIGEMAALETLDLSGNRFVGAIPDGISGCKNLVE-----VD 288
Qy 245 GSNNTVSG 252
Db 289 LSGNALTG 296
Search completed: May 9, 2005, 20:21:49
Job time : 68 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2005, 20:18:45 ; Search time 16 Seconds
(without alignments)
1605.617 Million cell updates/sec

Title: US-10-657-852A-15
Perfect score: 1385
Sequence: 1 MPEYNAKCCMLLVFLGLQ.....NTVSGSNHIVSGSNKVVTGD 267.

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues 283416
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	190.5	13.8	1008	2 D84434	probable receptor-
2	190	13.7	622	2 AF0169	probable exported
3	186	13.4	645	2 T05251	probable disease r
4	184.5	13.3	836	2 T46070	hypothetical prote
5	179.5	13.0	983	2 G84524	probable disease r
6	176.5	12.7	743	2 C84633	probable protein k
7	173.5	12.5	590	2 B86440	hypothetical prote
8	169	12.2	420	2 AE1857	hypothetical prote
9	168.5	12.2	1095	2 G96746	probable disease r
10	168	12.1	1019	2 C96519	probable disease r
11	164.5	11.9	716	2 H84421	probable receptor-
12	164	11.8	766	2 B85440	receptor kinase-li
13	162.5	11.7	1232	2 T05322	hypothetical prote
14	162	11.7	773	2 T00502	probable receptor-
15	161.5	11.7	905	2 T00475	probable disease r
16	161	11.6	719	2 T47727	hypothetical prote
17	161	11.6	907	2 A86460	99.9K hypothetical
18	159.5	11.5	768	2 T17462	disease resistance
19	158.5	11.4	658	2 B84664	probable receptor-
20	158	11.4	478	2 H86459	hypothetical prote
21	157.5	11.4	996	2 T10725	protein kinase Xa2
22	157	11.3	241	2 S61925	cyst wall protein
23	156.5	11.3	702	2 A86383	76.4K protein kina
24	156.5	11.3	876	2 D96558	probable protein k
25	156	11.3	371	2 T49908	hypothetical prote
26	156	11.3	638	2 T05606	protein kinase hom
27	155.5	11.2	942	1 JQ1674	protein kinase TMK
28	155	11.2	729	2 F86308	Similar to disease
29	154.5	11.2	1143	2 T10636	hypothetical prote

30	154	11.1	720	2 T02361	hypothetical prote
31	153	11.0	668	2 T05257	probable disease r
32	152.5	11.0	646	2 B84852	probable receptor-
33	152.5	11.0	655	2 G96524	protein T1N15.9 [i
34	152.5	11.0	838	2 A96557	probable receptor
35	152.5	11.0	980	2 H84632	probable receptor-
36	151.5	10.9	480	2 T00971	probable disease r
37	151	10.9	693	2 F96557	probable protein k
38	151	10.9	863	2 F85343	hypothetical prote
39	151	10.9	981	2 T50851	receptor protein k
40	150.5	10.9	221	2 T07079	leucine-rich repea
41	150.5	10.9	672	2 B84782	probable receptor-
42	150.5	10.9	813	2 T04313	protein kinase Xa2
43	149.5	10.8	286	2 C61615	sericin MG-2 - gre
44	149.5	10.8	645	2 E96631	probable receptor
45	149	10.8	976	2 B84659	probable receptor-

ALIGNMENTS

RESULT 1

D84434
probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: D84434
M.;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84434
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-1008 <STO>
A;Cross-references: GB:AE002093; NID:g6598459; PIDN:AAC78507.2; GSPDB:GN00139
C;Genetics:
A;Gene: At2g02220
A;Map position: 2

Query Match	13.8%;	Score	190.5;	DB	2;	Length	1008;
Best Local Similarity	27.5%;	Pred. No.	3e-06;				
Matches	68;	Conservative	45;	Mismatches	93;	Indels	41;
						Gaps	12;
QY	9	CMLLVFLG----	FILQVAGATSWSCHDDHLALGLAENLSGKGAVRLRAANS	GASCCSW	64		
Db	7	CVIVFLTELLCFFYSSSQTSRCHPHDLEALRDPFAHLEPKD	PGDWINSS-SSTOCCNW	65			
QY	65	EGVGCT-ASGRVVALRPKRGLGGIIPSSIGELDHLRYLDLSG	SLVGEVPKSLQIRLK	123			
Db	66	TDITCSNNTGVRVIRLEGLNKKLSGKLSGLKDEIRVLNLSR	NIKDSIPLSI-FNLK	124			
QY	124	SUTT---DSQSLGMSGINMLLVHSRRRTLDEPNTISGT----	NNS-----VGSGSNV	170			
Db	125	NLQTLDSLNDLS-GGIPTSINLPALQSPDLSSNFKNSLP	SHICHNSQIRVVLAVNY	183			
QY	171	VSGNDTVVSGNNHVSNSNTVVTGSDNTVVSNNHVS	GTKHIVTD-----NNNVVSGN	225			
Db	184	FAG-----NFTSGFKCVLL--EHLCLGMNDL----	TGNIPEDLPHLKLRLNLIGQ	228			
QY	226	DNNVSGS	232				
Db	229	ENRLSGS	235				

RESULT 2

AF0169
probable exported protein YP01388 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF0169

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, Nature 413, 523-527, 2001
 A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: AF0169
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-622 <KUR>
 A;Cross-references: UNIPROT:Q8ZGB5; GB:AL590842; PIDN:CAC90217.1; PID:G15979437; GSPDB:Q
 C;Genetics:
 A;Gene: YP01388

Query Match 13.7%; Score 190; DB 2; Length 622;
 Best Local Similarity 26.3%; Pred. No. 1.8e-06;
 Matches 68; Conservative 49; Mismatches 72; Indels 70; Gaps 13;
 QY 43 NLSGKGAVALRAAMSGACCCWEGVGCETASGRVVALRPLKGLGGLIPSSIGELDLRLY 102
 DB 41 NNNGNGTINIPDASNNDIHILTLGLNEQ-----LGGF-----SNHL-- 77
 QY 103 LDLSGNSLVGEVPSKQLRLKSLTDSQ-----SLMG-----SINMLLHVSS 145
 DB 78 IDSHNNTIDGQSNL-----VSSDGNMISALSLDGLFYGAQNTNLINNNLLIVTQ 131
 QY 146 RRT-LDEPNTISGNTNNSVSGSNVSGNDNTVVS-----GNNHVSNNNTV 193
 DB 132 GSTIDSNTVSGISNNLIESNNII--GNESCYSDDPASPAGMVCVDNQTLLGSDNNT 190
 QY 194 VTGSDNTVVGNNH--VVSQTKHIVTDNNNVVSGNDNVSGSFHTVS--GEHNTVSGSNNT 249
 DB 191 ITGALGNLHSHNDIIASSVNNLMDTHNIIAG-----GHYTISSGNNDFGSENN 244
 QY 250 VSGSNH1-VSGSNKVVTDG 267
 DB 245 VTDSTDMANGSNVVIDG 263

RESULT 3
 T05251
 probable disease resistance protein F18A5.210 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T05251
 R;Bevan, M.; Weber, N.; Gruening, D.; Schmidheini, T.; Bancroft, I.; Mewes, H.W.; Maye
 submitted to the Protein Sequence Database, February 1999
 A;Reference number: Z15405
 A;Accession: T05251
 A;Molecule type: DNA
 A;Residues: 1-645 <BEV>
 A;Cross-references: UNIPROT:Q9SVN1; EMBL:AL035528
 A;Experimental source: cultivar Columbia; BAC clone F18A5
 C;Genetics:
 A;Map position: 4
 A;Introns: 216/1; 541/1
 A;Note: F18A5.210

Query Match 13.4%; Score 186; DB 2; Length 645;
 Best Local Similarity 22.1%; Pred. No. 3.8e-06;
 Matches 82; Conservative 46; Mismatches 115; Indels 128; Gaps 14;
 QY 9 CMLAVFLGFILOVAGATSWSCCHDDLHALRGLAE-----NLSGKGAVALRAAW-SGAS 60
 DB 7 CLILSLNSKLVLAHVHKLRCQDKNALBFFKNEFYVHEFNNGIVGVKTEKWRNNTD 66
 QY 61 CCSWEGVGCETASGRVVALRL-----PKR-----GLGGLIPSSI 94
 DB 67 CCSWDGISCDPKTKGVVFLDLNNSFLNGLPLRYDSSLFLQLHLNLDLGSNNFSGILPDSI 126
 QY 95 GELDLRLYLDLSGNSLVGEVPSKQLRLKSLTDSQSL-----GMGSINML--LHV 143
 DB 127 GSKLYRLVSLGDCNLFQKIPSSLG-NLTYLTNLDLSVNDFTGELPDSMGHLNKLTELHL 185

QY 144 SSRTLDPEPNTISGTH--NSVSGSN-----NVVSGN-----DN 176
 DB 186 GSAKLGNSGFFMMLNLSELTLIDLSGNQFGNQTLYLDISANKIGQVFPQWLWLP 245
 QY 177 TVSGNNHVSQ-----SNNVTVTGSDNTVVS 204
 DB 246 QYVNISQNSFGPEGPADVIQRCGELMLDISNTFQDPFPLFNSTIFLGSNRRSGE 305
 QY 205 -----NHVSGTKHIVTDNN-----NVVSGNDNVSGSF--HTVSGEHN 241
 DB 306 IPKTKICKLVSLDTLVNNSNFNGSIPRCFEKFNFTLSVHLRNNNLSGPEESISDHLR 365
 QY 242 TVSGSNNTVSG 252
 DB 366 SLDVGRNRLSG 376

RESULT 4
 T46070
 hypothetical protein T18N14.120 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 16-Aug-2004
 C;Accession: T46070
 R;Delseny, M.; Berger, C.; Cooke, R.; Grellier, P.; Laudie, M.; Mewes, H.W.; Lemcke, K.;
 submitted to the Protein Sequence Database, December 1999
 A;Reference number: Z23013
 A;Accession: T46070
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-836
 A;Cross-references: UNIPROT:Q9SCT4; EMBL:AL132968
 A;Experimental source: cultivar Columbia; BAC clone T18N14
 C;Genetics:
 A;Map position: 3
 A;Introns: 625/1
 A;Note: T18N14.120
 C;Superfamily: protein kinase homology

Query Match 13.3%; Score 184.5; DB 2; Length 836;
 Best Local Similarity 25.7%; Pred. No. 6.7e-06;
 Matches 82; Conservative 48; Mismatches 100; Indels 89; Gaps 15;
 QY 10 MLVFLGFILOV-----AGATSW-----SCHDDHLALRGLAENLSKGNVRLRAWSG 58
 DB 22 LLICFLLPFSAQAVAGGGGGHSDGIVVTOANYQALQAIKHELIDFTG-----VLKSWNN 76
 QY 59 AS-----CCSWEGVGCETASGRVVALRPLKRGGLGGLIPSSIGELDLRLYLDLSGNSLVGEV 114
 DB 77 SASQVCSGWAGIKC--LRQGVVAIQLPWKGLGTISEKIGQLGSLRKLSHNNVIAVS 134
 QY 115 PKSLQIRLKS-----TTDSQSLGMSINMLHVSSRRRLDEPNTISGT----- 159
 DB 135 PRSLGY-LKSLRGVYLFNNRLSGSIPVSLGNCPL-----QNLDLSSNQLTGAIPPSLT 187
 QY 160 -----NNSVSGSNVSGNDNTVVSNNHVSQS--NNTVVTGS-----D 198
 DB 188 ESTRLYRLNLSFNSLSGLPLVPVARSYTLFDLQHNLSGSPDFFVNGSHPLKTLNLD 247
 QY 199 NTVVSGNHVSQTKHIVTDNNNVVSGNDNVVSGSFHTVSG-----EHNVTSGS-- 246
 DB 248 HNRFGAVPVSLCKHSLLEB---VSISHNQLSGSIPRECGGLPHQLQSLDFSYNSINGTIP 304
 QY 247 -----NNTVS-----GSNHI 256
 DB 305 DFSNLSLVSLLNLSNHL 323

RESULT 5
 G84524
 probable disease resistance protein [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

Query Match	12.7%	Score 176.5;	DB 2;
Best Local Similarity	26.7%	Pred. No. 2.3e-05;	
Matches 63:	Conservative	35;	Mismatches 81;
			Indels 57;
			Gaps 10;

Query Match	12.5%	Score	173.5;	DB	2;	Length	590;
Best Local Similarity	24.7%	Pred. No.	2.8e-05;				
Matches	70;	Conservative	44;	Mismatches	90;	Indels	79;
						Gaps	13;
Qy	5	MAKCCMLLVFGFLQVAGATSWSC	HHDLHARGLAENLSGKAVFLRAA	-----			55
Db	6	MKSCCSWLLIISLCSLINESQ	-----	AISPDGALLSFRNAVTRSDSFIH	51		
Qy	56	-W--SGASCCEWEGVCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSI	LVG	112			
Db	52	QMRBEDPPCWNWGTCDAKTRVTLNTYHKIMGPLPPDI	OKGLDHLRLMLHNNALYG	111			
Qy	113	EVPKSL-----QURLKS-LTTDSQSLGWSINMLLVSSRRRLDDEPNTISG	-----	158			
Db	112	AIPTALGNCTALEEHLQSNFYTGPIPAEWGDLPLG	-----	OKLDMSSNTLSGPIPASL	165		
Qy	159	-----TNNVSGSGSNVVVSGN--DNTVVS	GNNHNVSGSNNTVVTGSDNTVVGSGN	VSG	210		
Db	166	GQLKKLSNFNV-----SNNFLVGGIPSDGVLSG	-----	PSKNSFIGNINL	CG- 207		
Qy	211	TGHIUTDNNNVSGNDNNVSGSFHTVSG	HEHTNVSGSNNTVSGS	253			
Db	208	-KHV-----DVVCCDDSG-NPSSHSGSQGNQKNSGKLLIAS	243				

RESULT 8
AE1857
hypothetical protein all0406 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

```
Db      349 LSHLSLSSNNLLICEIPSSIGNLNQLTNFVGGNKLSGNLPATLSNLTNTKLTISLSSNQPT 408
              :|||::       :::::   :::::
QY      252 GS 253
              ||
Db      409 GS 410

RESULT 11
H84421
C;Species: Arabidopsis thaliana [mouse-ear cross] - Arabidopsis thaliana
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84421
R;Lin. X.; Kaul. S.: Rounslev. S.D.; Shea. T.P.; Benito. M.I.; Town. C.D.; Fritts
```


M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84421

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-716 <STO>

A;Cross-references: UNIPROT:Q9ZU46; GB:AB002093; NID:g4262228; PIDN:AAD14521.1; GSPDB:GN

C;Genetics:

A;Gene: At2g01210

A;Map position: 2

Query Match 11.9%; Score 164.5; DB 2; Length 716;

Best Local Similarity 27.4%; Pred. No. 0.00017;

Matches 63; Conservative 34; Mismatches 78; Indels 55; Gaps 9;

QY 10 MLIVFLGFILOVAGATSWCHDDHALRGLAENLSKGAVALRAAW--SGASCCSWGV 67

DB 1 MLASLIIFVALLCNVTIVISGLNDEGFALLTFKQSVHDDPTGSLN--WNNSDENACSWNGV 59

QY 68 GCTASGRVVALRPRKGLGGIIPSSIGELDLHRYLDLSGSLVGEVP-----KSL 118

DB 60 TCKEL--RVVSLIPRNLVYSLPSSIGELDLHRYLDLSGSLVGEVP-----KSL 117

QY 119 QI-----RLKSLTT--DSQSLGMSINM-LIHVSSRRRLDEEPTISGT-- 159

DB 118 VLVGNSFDGSLSEIGKLLQTLDSLQNLFNGLPLSLILQCNRLKTLDVSRNLSGPLP 177

QY 160 -----NNSVSGSNVNVSGNDNTVVGNNHVS 189

DB 178 DFGSAFVSLEKLDLAFNPQNGSPIDIGNL--SNLQGTADFSHNHTGS 225

RESULT 12

B85440

receptor kinase-like protein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004

C;Accession: B85440

R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A;Reference number: A85001; MUID:20083488; PMID:10617198

A;Accession: B85440

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-766 <STO>

A;Cross-references: UNIPROT:O23161; GB:NC_001268; NID:g7270708; PIDN:CAB80391.1; GSPDB:G

C;Genetics:

A;Gene: AT4g37250

A;Map position: 4

C;Superfamily: protein kinase homology

Query Match 11.8%; Score 164; DB 2; Length 766;

Best Local Similarity 28.5%; Pred. No. 0.0002;

Matches 63; Conservative 35; Mismatches 67; Indels 56; Gaps 9;

QY 60 SCSSWGVGCTASGRVVALRPRKGLGGIIPSSIGELDLHRYLDLSGSLVGEVPKSL- 118

DB 51 SPCSWRGISCNNDG--KVLTLSPNSQLLGSIPSDGLSLTLQSLDLSNNSFNGPLFVSFF 109

QY 119 ---QIRKSLTTDSQS---LGMGSTNMLLVSSRRRLDEEPTISGTNNVSGSNVV 171

DB 110 NARELFLDSLNNWISGEIPSAIGDLHNL-----TLNLSMDALA-----GKLPNTLA 157

QY 172 SGNDNTVSGNNHVSNNVVTGSDNTVVGSHVVGTKHIVTDNNNNVSG----- 224

DB 158 SLRNLTVSVLENNYFSGE-----IPGMRVV---BFLDLSNLSNLGSLPPDFG 202

QY 225 --NDNNVSGSFHTVSGE-----HNTVSGSNNTVSG 252

Db 203 GYSQYLVNVSFNQISGEIPPEIGVNPFRNVTVDLSFNLTG 243

RESULT 13

T05322

hypothetical protein F18P4.240 - Arabidopsis thaliana

N;Alternate names: hypothetical protein F1C12.60

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T05322; T04898

R;Bevan, M.; Terry, N.; Ardiles, W.; Buyssehaert, C.; Dasseville, R.; De Clerck, R.; De eves, H.W.; Mayer, K.F.X.; Schueller, C.

submitted to the Protein Sequence Database, April 1998

A;Reference number: Z15408

A;Accession: T05322

A;Molecule type: DNA

A;Residues: 1-1232 <BEV>

A;Cross-references: UNIPROT:Q9SN91; EMBL:AL022224

A;Experimental source: cultivar Columbia; BAC clone F1C12

R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.

submitted to the Protein Sequence Database, February 1998

A;Reference number: Z15388

A;Accession: T04898

A;Molecule type: DNA

A;Residues: 1-305 <BEW>

A;Cross-references: EMBL:AL021637

A;Experimental source: cultivar Columbia; BAC clone F18P4

C;Genetics:

A;Map position: 4

A;Introns: 863/1; 1116/1

A;Note: F1C12.60; F18P4.240

C;Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology; p

Query Match 11.7%; Score 162.5; DB 2; Length 1232;

Best Local Similarity 25.3%; Pred. No. 0.00045;

Matches 71; Conservative 41; Mismatches 94; Indels 75; Gaps 11;

QY 11 LVLVFLGFILOVAGATSWCHDDHAL-----RGLAENLSKGAVALRAAWS--GASCCSW 64

DB 4 LVLLLLFILCFSGSLGQPGIINNDLQTLLEVKKSLVTNPQDDPLR---QWNSDNIYCSW 60

QY 65 EGVGCE-TASGRVVALRPRKGLGGIIPSSIGELDLHRYLDLSGSLVGEVPKSLQIRLK 123

DB 61 TGVTCDNTGLFRVIALNLTLGLTGSISPMFCRFDNLHLDLSSNLLVGPITALS-NLT 119

QY 124 SLTTDSQSLGMSINMLLVSSRRRLDEEPTISGTNN--SVGSGSNVNVSGNDNTVVG 181

DB 120 SLES-----LFLFSNQLTGEIPSQLGSLVNRSLRIGDNLVGDIPETL--G 164

QY 182 N-----NNHVSG-----SNNTVVTGSD 198

DB 165 NLVNLQMLALASCRLTGPIPSQLGRVRYOSLIQDNYLEGPPIPAELGNCSDLTVTAAE 224

QY 199 NTVVSGNHVVGTKHIVTDNNNVSGNDNNVSGSFHTVSGE 239

DB 225 NMLNGTIPAEIQR-----LENLEILNANSLTGEIPSQLGE 261

RESULT 14

T00502

probable receptor-like protein kinase At2g23300 [imported] - Arabidopsis thaliana

N;Alternate names: protein kinase homolog T20D16.7

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Aug-2004

C;Accession: T00502; A84623

R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, submitted to the EMBL Data Library, November 1997

A;Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.

A;Reference number: Z14164

A;Accession: T00502

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-773 <ROU>

A;Cross-references: UNIPROT:O22178; EMBL:AC002391; NID:g2642427; PID:g2642433

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: T00475

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-773 <STO>

C;Cross-references: GB:AE002093; NID:g2642433; PIDN:AAB87101.1; GSPDB:GN00139

C;Genetics: F84762

A;Gene: AC293300; T20D16.7

A;Map position: 2

A;Introns: 545/1

C;Superfamily: protein kinase homology

Query Match 11.7%; Score 162; DB 2; Length 773;
Best Local Similarity 27.3%; Pred. NO. 0.00028;
Matches 66; Conservative 36; Mismatches 86; Indels 54; Gaps 8;

QY 26 SMSCHRDDLHALRGLAENLSGKAVRLRAAWGASCCSWEGVGCETACGRVVALRLPKRG 85
Db 55 SNNYDHD-----NFCSWRGVLCNDS-RVVTLSLPNSN 86

QY 86 LGGIIPSSIGELDHLRYLDLSGNLSIVGPKSL-----QIRKLSTYDSQS----LGMGSI 137
Db 87 LVGSIPIFDLGLQNLQSLNLSNLSGLPVFFAADKLRFLDLSNLSIGEIPVSI 146

QY 138 NMLLHVSSRRTIDEDEPTTISGTNNVSGSGNNVSGNDNTVTVSGNNHVSGNNVTVTGS 197
Db 147 HNL-----QTLNLSNIFTKLPA-----NLASGLSTELSKKNYSGFPGGWRK 194

QY 198 DNTVGSNNHVSGT--KHIVTNNVSGNDNNVSGSFHTVSG----EHTVSGSNNTVS 251
Db 195 VQVLDISNLSLNGSLPPDFSGDNLRLVNSYNQISGEIPPNVGAGPQATVDFSFNNLT 254

QY 252 GS 253
Db 255 GS 256

RESULT 15

T00475

probable disease resistance protein [imported] - Arabidopsis thaliana

N;Alternate names: hypothetical protein F1913.16

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C;Accession: T00475; F84762

R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, April 1998

A;Description: Arabidopsis thaliana chromosome II BAC F1913 genomic sequence.

A;Reference number: Z14160

A;Accession: T00475

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-905 <ROU>

A;Cross-references: UNIPROT:O64757; EMBL:AC004238; NID:g3033373; PID:g3033389

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: F84762

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-905 <STO>

A;Cross-references: GB:AE002093; NID:g3033389; PIDN:AAC12833.1; GSPDB:GN00139

C;Genetics:

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2005, 20:15:44 ; Search time 43 Seconds
(without alignments)
463.519 Million cell updates/sec

Title: us-10-657-852a-15

Perfect score: 1385

Sequence: 1 MPEYMAKCMMLVFLGLFILO.....NTVSGNHNIVSGSNKVVTGD 267

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*

2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182	13.1	941	3	US-09-336-447A-9
2	182	13.1	941	4	US-09-952-267B-9
3	177	12.8	892	3	US-09-336-447A-5
4	177	12.8	892	4	US-09-952-267B-5
5	176.5	12.7	804	4	US-10-101-464A-890
6	175	12.6	889	3	US-09-336-447A-15
7	175	12.6	889	4	US-09-952-267B-15
8	174	12.6	843	4	US-10-101-464A-893
9	171.5	12.4	323	4	US-10-101-464A-764
10	170.5	12.3	386	4	US-10-101-464A-902
11	170.5	12.3	707	3	US-09-228-986-80
12	170.5	12.3	707	4	US-10-101-464A-80
13	170	12.3	624	3	US-09-336-447A-7
14	170	12.3	624	4	US-09-952-267B-7
15	168.5	12.2	187	4	US-10-101-464A-732
16	164	11.8	828	4	US-10-101-464A-934
17	163	11.8	692	4	US-10-101-464A-897
18	158	11.4	942	4	US-10-101-464A-911
19	155	11.2	867	4	US-09-540-236-2676
20	153	11.0	653	4	US-10-101-464A-953
21	152	11.0	224	4	US-10-101-464A-770
22	152	11.0	257	4	US-10-101-464A-743
23	150.5	10.9	864	4	US-10-101-464A-896
24	150	10.8	666	3	US-09-228-986-68
25	150	10.8	666	4	US-10-101-464A-68
26	150	10.8	998	4	US-10-101-464A-914
27	149.5	10.8	645	4	US-09-345-473B-15

28	149.5	10.8	645	4	US-09-345-473B-16	Sequence 16, Appl
29	149.5	10.8	873	3	US-09-336-447A-13	Sequence 13, Appl
30	149.5	10.8	873	4	US-09-952-267B-13	Sequence 13, Appl
31	149	10.8	878	4	US-09-540-236-3401	Sequence 3401, Ap
32	147.5	10.6	711	3	US-09-228-986-79	Sequence 79, Appl
33	147.5	10.6	711	4	US-10-101-464A-79	Sequence 79, Appl
34	147.5	10.6	910	3	US-09-228-986-72	Sequence 72, Appl
35	147.5	10.6	910	4	US-10-101-464A-72	Sequence 72, Appl
36	146.5	10.6	635	4	US-10-101-464A-932	Sequence 932, App
37	146	10.5	831	3	US-09-336-447A-1	Sequence 1, Appl
38	146	10.5	831	4	US-09-952-267B-1	Sequence 1, Appl
39	145.5	10.5	160	4	US-10-101-464A-772	Sequence 772, App
40	145.5	10.5	370	4	US-10-101-464A-944	Sequence 944, App
41	143.5	10.4	659	3	US-09-228-986-75	Sequence 75, Appl
42	143.5	10.4	659	4	US-10-101-464A-75	Sequence 75, Appl
43	143	10.3	144	4	US-10-101-464A-739	Sequence 739, App
44	142.5	10.3	655	3	US-09-228-986-70	Sequence 70, Appl
45	142.5	10.3	655	4	US-10-101-464A-70	Sequence 70, Appl

ALIGNMENTS

RESULT 1
US-09-336-447A-9
; Sequence 9, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336,447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-9

Query Match 13.1%; Score 182; DB 3; Length 941;
Best Local Similarity 34.2%; Pred. No. 1e-08;
Matches 39; Conservative 19; Mismatches 50; Indels 6; Gaps 1;
QY 154 NTISGTNNVSGSGNNVSGNDNTVVGNNHVVSGSNTVVTGSDNTVVGNNHVVSGTKH 213
Db 123 NEAMGEYTVAGANNQAKGNTVVGNGNKAIGNNTVVGSGNNQAKGEHSTIAGK- 181
QY 214 IVTDNNVVGNDNNVVGSGFHTVSGEHTVVGNNHVVSGSNTVVGNNHVVSGKVVTGD 267
Db 182 -----NNQATGNGSFAAGVENKADANNAVALGNKTIEGTNSVAIGSNNTVTKG 230

RESULT 2
US-09-952-267B-9
; Sequence 9, Application US/09952267B
; Patent No. 6753417
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/952,267B

; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/336,447
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-952-267B-9

Query Match 13.1%; Score 182; DB 4; Length 941;
Best Local Similarity 34.2%; Pred. No. 1e-08;
Matches 39; Conservative 19; Mismatches 50; Indels 6; Gaps 1;
Qy 154 NTISGNSVSGSNVSGNDNTVSGNNHVSNNNTVTGSDNTVVGSHVSGTKH 213
Db 123 NEAMGEYTVAGGANNQAKGNYSTVGGGNGKNAIGNNSTVVGSGNNAQGEHSTIAGGK- 181
Qy 214 IVTDNNVSGNDNNVSGSFHTVSGEHTVSGNNTVSGNNHVSNNKVVTDG 267
Db 182 -----NQATGNGSPAAGVENKADANNAVALGNKNTIEGTSVAIGSNNTVKTG 230

RESULT 3
US-09-336-447A-5
; Sequence 5, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USP41 AND USP42 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336,447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 892
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-5

Query Match 12.8%; Score 177; DB 3; Length 892;
Best Local Similarity 31.8%; Pred. No. 2.9e-08;
Matches 35; Conservative 20; Mismatches 49; Indels 6; Gaps 1;
Qy 158 GTNSVSGSNVSGNDNTVSGNNHVSNNNTVTGSDNTVVGSHVSGTKHIVTD 217
Db 143 GDSSTIGGYNQATGEKSTVAGGRNQATGNNSTVAGGSYNQATGNNSTVAGGSH----- 198
Qy 218 NNNVSGNDNNVSGSFHTVSGEHTVSGNNTVSGNNHVSNNKVVTDG 267
Db 199 --NQATGGSFAGVENKANNANNAVALGNKNTIDGNSVAIGSNNTIDSG 246

RESULT 4
US-09-952-267B-5
; Sequence 5, Application US/09952267B
; Patent No. 6753417
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USP41 AND USP42 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024

; CURRENT APPLICATION NUMBER: US/09/952,267B
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/336,447
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 892
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-952-267B-5

Query Match 12.8%; Score 177; DB 4; Length 892;
Best Local Similarity 31.8%; Pred. No. 2.9e-08;
Matches 35; Conservative 20; Mismatches 49; Indels 6; Gaps 1;
Qy 158 GTNSVSGSNVSGNDNTVSGNNHVSNNNTVTGSDNTVVGSHVSGTKHIVTD 217
Db 143 GDSSTIGGYNQATGEKSTVAGGRNQATGNNSTVAGGSYNQATGNNSTVAGGSH----- 198
Qy 218 NNNVSGNDNNVSGSFHTVSGEHTVSGNNTVSGNNHVSNNKVVTDG 267
Db 199 --NQATGGSFAGVENKANNANNAVALGNKNTIDGNSVAIGSNNTIDSG 246

RESULT 5
US-10-101-464A-890
; Sequence 890, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 890
; LENGTH: 804
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-890

Query Match 12.7%; Score 176.5; DB 4; Length 804;
Best Local Similarity 23.4%; Pred. No. 2.8e-08;
Matches 77; Conservative 54; Mismatches 105; Indels 93; Gaps 13;
Qy 10 MLLVFLGFI-----QVAGATSWSCHD--DIHALRGLAE--NL 44
Db 6 LLLVMGVAMPTHSQHTGGFTSVQFPFNGRSMGKPSIAGYHEKRDVEALLSPKGI 65
Qy 45 SGKAVRLRAAWGASCCSWEGVCETASGRVVALRIPKRGIGIIPSSIGELDLHVLVD 104
Db 66 DPYGLSNWTANNHNVCLWNGISCSPTNRVVEISRYRLNGLTSPYIGNLSLLRLHD 125
Qy 105 LSGNSLVGEVPKSL-----QIRLKSLLTDSOS-----LGMGSINMLLHVSRRTLDEPN 154
Db 126 LSSNALSGRIPAEFGQLKALRIILDSNNALTGSIPTCIGNGLGNTL-----DLDLN 179
Qy 155 TISG-----TNSVSGSNVSGNDNTVSGNN--NHVSGSNNTV- 194
Db 180 AFSGRIPKELFNCTRLQRLIDLSHNSL-TGSIPTSIGNCALLQTLNTGNYLSGSIPTSLA 238

```

Qy      195  --TGSDNTVVGSHV-----VSGTKHIVTDNRNV-----VSGND 226
          :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db      239  NCTSTDLVISNNLSGPIPFEGGLVSLKFLFLDDNSISGSIPTSLVNCTSLFALKGSG 298
          :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Qy      227  NNVSQSFTVSG---EHNVTGSGNNNTVSG 252
          :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db      299  NKLSGPIPSVMGLMKISITIDLNNSLTG 327
          :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:

RESULT 6
US-09-336-447A-15
; Sequence 15, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FRENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336.447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 889
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-15

```

Query Match	12.6%	Score 175;	DB 3;	Length 889;
Best Local Similarity	27.1%;	Pred. No. 4.5e-08;		
Matches	49;	Conservative 25;	Mismatches 66;	Indels 38; Gaps 5;
Qy	126	TTDSQSIGMGSINMLLHVSS-----RRTLDSEPNTIS-CTNNNSVSGSNVV	171	
Db	184	TGESSTVAGGNNILAEKSKSAIGGRQNEASGDRSTVSGGYNNIAEKKSAIGGGEPFLA	243	
Qy	172	SGNDNTVVGNNNHVSGSNNTTGTGSDNTVVGSNHHVSGTK--HIVTDNNNVSGDNNV	229	
Db	244	LGNWATISGRQNEASGDRSTVAGGEQNQAIGKYVTISGGQRNEASGDRSTVAGGEQNQA	303	
Qy	230	SGSFHTVSGEH-----NTVS-GSNNTVSGSNHIVSGSNKV	264	
Db	304	IGKYTSVSGGYRNQATGKGFPAAGIDNKANADNAVALGNKNTTEGENSVAGISNNTV	360	

RESULT 7
US-09-952-267B-15
; Sequence 15, Application US/09952267B
; Patent No. 6753417
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USP41 AND USP42 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/952,267B
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/336,447
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 889
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis

```

US-09-952-267B-15

Query Match      12.6%; Score 175; DB 4; Length 889;
Best Local Similarity 27.1%; Pred. No. 4.5e-08;
Matches 48; Conservative 25; Mismatches 66; Indels 38; Gaps 5;

QY      126  TTDSQSIGMSGINMLLHVSS-----RRTLDEEBNTTIS-GTNNVSGSGNNVV 171
      | : : : | : : | : | : | : : : | : : | : : : | : : | :
DB      184  TGESSTVAGGSNNLAEKGSSAIGGGRQNEASGDRSTVSGGYNNLAEKGSSAIGGGEFNLA 243
      | : : : | : : | : | : | : : : | : : | : : : | : : | :
QY      172  SGNDNTVVSGNNHVSGNNNTVVTGSDNTVVVSGNNHVSGTK--HIVTDNNNVSGNDNNV 229
      | : : : | : : | : | : | : : : | : : | : : : | : : | :
DB      244  LGNNATISGGRQNEASGDRSTVAGEQNOALGKYSTISGGGRQNEASGDRSTVAGEQNOA 303
      | : : : | : : | : | : | : : : | : : | : : : | : : | :
QY      230  SGSFHTVSGEH-----NTVSGSNNTVSGSNHIVSGSNKV 264
      | : : : | : : | : | : | : : : | : : | : : : | : : | :
DB      304  IGYKSTVSGGYRNQATGKGSFAAGIDNKANADNAVALGNKNTIEGNSVAIGSNNTV 360
      | : : : | : : | : | : | : : : | : : | : : : | : : | :

RESULT 8
US-10-101-464A-893
; Sequence 893, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101.464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 893
; LENGTH: 843
; TYPE: PRT
; ORGANISM: Pinus radiata
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(843)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-101-464A-893

```

Query Match	12.6%;	Score 174;	DB 4;	Length 843;
Best Local Similarity	22.7%;	Pred. No. 5.2e-08;		
Matches	80;	Conservative 55;	Mismatches 107;	Indels 110; Gaps 13;
QY	13	VFLGFIQLQVAGATSWSC-----HDDLDHALRGLAENLSGK--GAVRLRAAAWSGASCC	62	
Db	15	VMMGVAMPTDGTFSVESVPENGRNRHRKRDVEALLSPKESIIDSPYGSILTNWTANNSHVC	74	
QY	63	SWEGVGGETASGRVVALRLPKRGLGGIIPSGIGELDHLRYLDLSCNSILVGEVPKSLQIRL	122	
Db	75	LWNGISCRPNTRKRVVISLPECWLNGTLSPYIGNLSLRHLRDLDSWNAISGRIPAEFG-QL	133	
QY	123	KSLATTDQSQSLGWSGIN-----MLLHVSSRRTLDEPNTISGT--NNSVGSGS-----	167	
Db	134	KALRILDLSHGLLHGVIPEKLFNCTRQLQRIDLSHNSFTGSIPTSIGNSALLQTMNLAE	193	
QY	168	-----NNVTVSG-----NDNTVVSG-----	181	
Db	194	NOLRGSIPAEGRVLVHLESQLQVNTLSUGSIPTSLANCTSLLIKLELSDNN--LSGPIIPSEP	252	
QY	182	-----NNNHVSGSNNTTVTG-----SDNTVVGSHNVSGTKHIVTDNNV	221	

```
Db 253 SRLVLETLFPDNGISGIPASISNCTSLQYLDISDNLSP-----IPSEFRL 303
QY 222 VS-----GNDNVSGSFHTVGEHNTVS---GNNVTGSGNHIIVSGSNKVV 265
Db 304 VSLESYFDHNSIGSIPFTLVNCTSLSGALGASGNKLSGSPSVNGLMKNIS 355

RESULT 9
US-10-101-464A-764
; Sequence 764, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 764
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-764

Query Match 12.4%; Score 171.5; DB 4; Length 323;
Best Local Similarity 25.5%; Pred. No. 2.4e-08;
Matches 82; Conservative 52; Mismatches 112; Indels 75; Gaps 14;

QY 10 MLLVFLGIL-----QVAGATSWCHD--DLHALRGLAE--NL 44
Db 6 LLLVMGVAMPHTHSQHTGFTSVQFPFNGRSMGMKPSIAGYHEKRDVEALLSPKGT 65
QY 45 SGKGAVALRAWSGASCCSWEGVGCETASGRVALRLPKRGLGIIPISSIGELDLHYLD 104
Db 66 DPYGLSNWNTANNHNVCLMNGISCPNTRVWEISRYGRNLGTLSPYIGNLSLRHLD 125
QY 105 LSGNSLVGEVPKSL---QIRLKSITTDQS-----LGMGSINMLLHVSRRTLDDEPN 154
Db 126 LSSNALSGRIPAEFGQKALRIIDLNNALTGSIPTCIGNGLGNTL-----DLDSLWN 179
QY 155 TISG-----TNNVSGSGNNVSGNNTVTVSGNN--NHVSGSNNTVV- 194
Db 180 AFSGRIPKELFNCTRLQRIIDLHNSL-TGSIPTSGNCALLQTLNTPGNVLSGSIPTSLA 238
QY 195 --TGSNDTVGSHVSGTKHIVTDNNVVS-----GNDNVSGSFHTVGEHNT---VS 244
Db 239 NCTSLTDLVIVSSNN--LSGP--IPSEFSLVSLKFLFDNDNISGISIPTSLVNCITSLFALK 295
QY 245 GSNNTVSGNHIIVSGSNKVV 265
Db 296 GSGNKLSPGPSVGLMKSIS 316

RESULT 10
US-10-101-464A-902
; Sequence 902, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
```

```
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 902
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-902

Query Match 12.3%; Score 170.5; DB 4; Length 386;
Best Local Similarity 32.3%; Pred. No. 3.8e-08;
Matches 52; Conservative 25; Mismatches 61; Indels 23; Gaps 7;

QY 29 CHHDDLHALRGLAENLSGKGAVALRAAWS--GASCCSWEGVGCETASGR---VVALRLPKR 84
Db 38 CNOQSDVQALISFKQTVSSSSPLN---WEVNRSCCTWEGVTCGLLSLQFQSVTKRLPGR 93
QY 85 GLGGIIPSSIGELDLHYLDLSGNSLVGEVPKSLQIRLKSITTDQSILGMSINMLLHV- 143
Db 94 RLRTLSDSLGRLAHLREINVSFNLITGEVGRFL-LQHL--EVLDSLNNLSVIAPIA 150
QY 144 ---SSRETLDEEPNTISGTNNVSGS-----SNNVSG 173
Db 151 QGLNSIRTFNISNSFRGNVPQLGSAVNLTSEFVNSNNSFTG 191

RESULT 11
US-09-228-986-80
; Sequence 80, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-80

Query Match 12.3%; Score 170.5; DB 3; Length 707;
Best Local Similarity 26.1%; Pred. No. 8.9e-08;
Matches 81; Conservative 39; Mismatches 89; Indels 101; Gaps 16;

QY 9 CMLLVFLGFILOVA---GATSWCHDDHLHALRGLAENLSGKGAVALRAAWS--GASCC- 62
Db 8 CLRILITAILTASIALSHGTTD----PDDVSALKGIYSLNSPOOL---SGWSANGGDP 60
QY 63 -SWEGVGCETASGRVVALRLPKRGLGIIPISSIGELDLHYLDLSGNSLVGEVPKSLQIR 121
Db 61 QSWKGVSCGSS--VTILKLSGLSGSLYYQLSDLSLTLTDLSDNNIQTNPYALPQK 118
QY 122 LKSLITTDQSILGMSI-----NM-----LLH-----VSSRRTLDEEPNTI 156
```

```

Db      119  LOELNLASNGLS-GTIPYISINMTGLTDLKLSHNLQSGQIQDIFQQLSLSLTLDLSFNWTL 177
Qy      157  SGT-----NNSVSGSGNNVSVSGNDNTVVSNNHVS----- 188
Db      178  TQNLPLQPSFSSLSLSVLYLQNNQL-AGSVNVLANLPLTDLNTENNRFSGWPNVWRSNQ 236
Qy      189  ----SNNVTVG-----SDNTVVSNSHV---SCTKHIVTDNNNVSGNNDN 228
Db      237  FKYSGSGNSFATGPAPPPPPYTPPPPSNNRPPKSSNVVPSSGSGK-----GGSNKK 286
Qy      229  VSGSFHTVS 238
Db      287  KSLSGGAIVG 296

RESULT 12
US-10-101-464A-80
; Sequence 80, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 707
; TYPE: FRT
; ORGANISM: Pinus radiata
US-10-101-464A-80

```

```

RESULT 13
US-09-336-447A-7
; Sequence 7, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPAl AND USP2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336,447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-7

Query Match 12.3%; Score 170; DB 3; Length 624;
Best Local Similarity 30.6%; Pred. No. 8.3e-08;
Matches 38; Conservative 24; Mismatches 50; Indels 12; Gaps 2

Qy 154 NTISGTNNVSGSGNNVTVSGNDNTVTVSGNNHVSNNNTVTVGSDNTVVGSHVVSCTKH 213
Db 104 NOAKGEHSITAGGESNOATGRNSTVAGGSNNQAVGTNSTVAGGSNNQAKGANSFAAGVGN 163
Qy 214 IVTDNNNVSGNDNNVSGSFHTVSGEHTVSG-----GSDNTVSGSNHIVSG---SN 261
Db 164 QANTDNAVGKNTTNGNNSAIGSENTVNEKQNVILGSDNTTNAQGSVLLGHETSG 223
Qy 262 KVVT 265
Db 224 KEAT 227

RESULT 14
US-09-952-267B-7
; Sequence 7, Application US/09952267B
; Patent No. 6753417
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPAl AND USP2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/952,267B
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/336,447
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-952-267B-7

```

Query Match	12.3%	Score 170;	DB 4;	Length 524;
Best Local Similarity	30.6%;	Pred. No. 8.3e-08;		
Matches 38;	Conservative 24;	Mismatches 50;	Indels 12;	Gaps 2;
Qy	154	NTTSGTNNVCGSGSNNTVVGSGNDNTVVGSGNNHNVGSGNNTVVGSGDNTVVGSGNHVVGSGTGH	213	
db	104	NOAKGEHSTTAGGGSNOATGNSNTVAGGSNNCOATGNTSTVAGGSNNOKAGNSFAAGVGN	163	

Search completed: May 9, 2005, 20:22:40
Job time : 49 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2005, 20:21:56 ; Search time 138 Seconds
(without alignments)
645.441 Million cell updates/sec

Title: US-10-657-852a-15

Perfect score: 1385

Sequence: 1 MPEYAKCMLLVLFLGLQ.....NTVSGNHVSGSKVVTDG 267

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1428581 seqs, 333598853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/prodata/2/pubpaa/US05_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
 - 10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
 - 11: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
 - 12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/prodata/2/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	262	18.9	1010	16 US-10-437-963-180288	Sequence 180288,
2	206.5	14.9	1039	16 US-10-437-963-166082	Sequence 166082,
3	204	14.7	1021	15 US-10-443-101-2	Sequence 2, Appli
4	198	14.3	284	16 US-10-437-963-148813	Sequence 148813,
5	197	14.2	961	16 US-10-437-963-172660	Sequence 172660,
6	194	14.0	917	16 US-10-437-963-115627	Sequence 115627,
7	194	14.0	1164	16 US-10-437-963-192784	Sequence 192784,
8	192.5	13.9	838	16 US-10-437-963-169754	Sequence 169754,
9	192	13.9	1060	16 US-10-437-963-153194	Sequence 153194,
10	190	13.7	1044	16 US-10-437-963-162505	Sequence 162505,
11	188.5	13.6	1011	16 US-10-437-963-172329	Sequence 172329,
12	188.5	13.6	1078	16 US-10-437-963-123119	Sequence 123119,
13	186	13.4	278	15 US-10-424-599-267766	Sequence 267766,

14	186	13.4	676	16	US-10-437-963-153306	Sequence 153306,
15	185	13.4	1012	16	US-10-437-963-192786	Sequence 192786,
16	183.5	13.2	380	16	US-10-437-963-136619	Sequence 136619,
17	183.5	13.2	1133	16	US-10-437-963-150876	Sequence 150876,
18	183.5	13.2	1140	16	US-10-437-963-119802	Sequence 119802,
19	182	13.1	941	10	US-09-952-267-9	Sequence 9, Appli
20	182	13.1	1231	16	US-10-437-963-102913	Sequence 102913,
21	181	13.1	653	15	US-10-389-566-1625	Sequence 1625, Ap
22	181	13.1	1065	16	US-10-437-963-109994	Sequence 109994,
23	181	13.1	1469	16	US-10-437-963-196963	Sequence 196963,
24	180.5	13.0	675	16	US-10-437-963-174437	Sequence 174437,
25	180	13.0	1036	16	US-10-437-963-149679	Sequence 149679,
26	180	13.0	1080	16	US-10-437-963-110291	Sequence 110291,
27	179	12.9	516	15	US-10-424-599-201138	Sequence 201138,
28	178	12.9	153	15	US-10-425-114-63986	Sequence 63986, A
29	178	12.9	792	16	US-10-437-963-109998	Sequence 109998,
30	178	12.9	1051	16	US-10-437-963-156545	Sequence 156545,
31	177.5	12.8	470	16	US-10-437-963-172330	Sequence 172330,
32	177.5	12.8	990	16	US-10-437-963-170216	Sequence 170216,
33	177	12.8	892	10	US-09-952-267-5	Sequence 5, Appli
34	176.5	12.7	804	14	US-10-101-464A-890	Sequence 890, App
35	176.5	12.7	804	17	US-10-864-252-890	Sequence 890, App
36	176.5	12.7	817	16	US-10-437-963-114827	Sequence 114827,
37	176	12.7	852	15	US-10-282-122A-62892	Sequence 62892, A
38	175.5	12.7	1036	16	US-10-437-963-157688	Sequence 157688,
39	175	12.6	889	10	US-09-952-267-15	Sequence 15, Appl
40	175	12.6	1000	16	US-10-437-963-138726	Sequence 138726,
41	174.5	12.6	556	16	US-10-437-963-109997	Sequence 109997,
42	174.5	12.6	967	16	US-10-437-963-118888	Sequence 118888,
43	174.5	12.6	1060	16	US-10-437-963-167059	Sequence 167059,
44	174	12.6	344	16	US-10-437-963-158951	Sequence 158951,
45	174	12.6	843	14	US-10-101-464A-893	Sequence 893, App

ALIGNMENTS

RESULT 1

US-10-437-963-180288
; Sequence 180288, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 180288
; LENGTH: 1010
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_7766C.1.pep
US-10-437-963-180288

Query Match 18.9%; Score 262; DB 16; Length 1010;
Best Local Similarity 40.1%; Pred. No. 18; 13;
Matches 71; Conservative 19; Mismatches 53; Indels 34; Gaps 5;
QY 7 KCML-LVPLGLQVAGATSWSCCHDDLHLRLAENLS-GKGAVLRAAWSGSCCSW 64
DB 8 RCLFSLVAFLLPPPPAAAAPCPEDLALRAFAGNLSAGGGGAGLRAWSGDACCW 67
QY 65 EGVGCTASGRVVALRPRKGLGGIIPSSIGELDLRLYLDLGNLSVGEVPSLQIRLS 124

Db 68 DGVACD-RAARVTALRPGLEGIPPSLAALRQDLDSHNALT-----113
QY 125 LTTDSQSLGMSINMLLVHSSRRTLDEEPTISGT-----NNSVGGSGNNVVSG 173
Db 114 -----GGISALLAAVSLRTANLSSNLLNDTLDLAALPHLSAFNASNLSLG 160

RESULT 2

US-10-437-963-166082
; Sequence 166082, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 166082
; LENGTH: 1039
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_64826C.1.pap
US-10-437-963-166082

Query Match 14.9%; Score 206.5; DB 16; Length 1039;
Best Local Similarity 29.1%; Pred. No. 6.6e-09;
Matches 83; Conservative 52; Mismatches 103; Indels 47; Gaps 13;
QY 5 MAKCCMLVFGFIQV--AGATSWCHDDHDLHALRGLAENLSGKGVRLRAAWSGAS-C 61
Db 1 MARAMALLFCYALALYSAGSSSSSNATADALALLSPKSLSSP-SIGLMASWNSSHF 59
QY 62 CSWEGVGCETAS-GRVVALRPLKRGGLGIIIPSSIGELDLHRYLDLSGNSLVGVPKSL-- 118
Db 60 CSWTGVCSCROQPEKVIQALQNSCGLSRIIPFICNLISFLKTLQGNQLVQGPSELGH 119
QY 119 --QIRLKSLLTDSQSLGMSIN-----MLLVHSSRRTLDEEPTI-SGTNNVSGSG 166
Db 120 LSKRLMLNST---NLLRGSIPVEMRGCTKLMTLHLGNQLQGEIPAEIGSSLKLNLY 176
QY 167 -SNNVSGN-----DNTVSGNNHVSNNVTVTGSDN--TVVGSNNHVS--T 211
Db 177 LTRNLLSGEIPQSLAEPLSLELLSHNKLSGEVPALSNTLTNLNTRFSNNMLSGVIPS 236
QY 212 KHIVTDNNVSGNDNNVSG-----SFHTVSGEHNVTSGS 246
Db 237 SLGMLPNLYELSLGFNNLSGPIPTSIWNISLRALSVOGNMLSGT 281

RESULT 3

US-10-443-101-2
; Sequence 2, Application US/10443101
; Publication No. US20040096941A1
; GENERAL INFORMATION:
; APPLICANT: MATSUBAYASHI, YOSHIKATSU
; APPLICANT: SAKAGAMI, YUJI
; TITLE OF INVENTION: RECEPTOR FOR PLANT CELL GROWTH FACTOR
; FILE REFERENCE: 238013USO
; CURRENT APPLICATION NUMBER: US/10/443,101
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: JP 2002-335572
; PRIOR FILING DATE: 2002-11-19

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1021
; TYPE: PRT
; ORGANISM: Daucus carota
US-10-443-101-2

Query Match 14.7%; Score 204; DB 15; Length 1021;
Best Local Similarity 24.6%; Pred. No. 1.1e-08;
Matches 81; Conservative 56; Mismatches 94; Indels 98; Gaps 14;

QY 10 MLLVFLGFIQ--VAGATSWCHDDHDLAL-----RGLAENLSGKGVRLRAAWS----- 57
Db 8 VILLVGFQVIVVNSQNTCSNDLKALEGFMRGLESSIDG-----WKWNESSS 58
QY 58 -GASCCSWEGVGCETA-----SGRVVALRPLKRGGLGIIIPSSIGELDLHRYLDLS 106
Db 59 FSSNCCDWGIGISCKSVSLGLDDVNESGRVVELEGRRLSGKLSVAKLDQLKVLNLT 118
QY 107 GNSLVGVPKSL-----QIRLKSLLTDSQSLGMSINMLLVHSSRRTLDEEPTISG----- 158
Db 119 HNSLGSIAASLLNLSLEVLDSNDPS---GLFPSLNLPLSLRVLVNVYENSFHLIPA 175
QY 159 --TNN-----SVGSGSNNVSGNDNTV--VSGNNHVS-----SNNTVV 194
Db 176 SLGNLPRIRIDLAMNYFDGSPVIGICNCSSVEYIGLASNNLSGSPQELFQLSNLSVL 235
QY 195 TGSNTVTVGSNNHVSQTKHIVTDNNVSGNDNNVSGSFHTV-----SGEHNVTVS 244
Db 236 ALQNNRLSGA---LSSKLGKLSNLGRDLISSNKFCKIPDVFLKLNKLVYFSAQSNLFN 291
QY 245 GS-----NNTVSGSNHI 256
Db 292 GEMPRSLNSRSISLLSLRNNLTSLGGIYL 320

RESULT 4

US-10-437-963-148813
; Sequence 148813, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 148813
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_49206C.1.pap
US-10-437-963-148813

Query Match 14.3%; Score 198; DB 16; Length 264;
Best Local Similarity 27.6%; Pred. No. 6.2e-09;
Matches 70; Conservative 42; Mismatches 116; Indels 26; Gaps 8;
QY 5 MAKCCMLVFGFIQVAGATSWCHDDHDLHALRGLAENLSGKGVRLRAAW-SGASCCS 63
Db 1 MQELQLLLVLAALVLSFLSPATSCTEQEKSSLLQFLRELSPDSSSKFSRWSQSGTSCCT 60
QY 64 WEGVGCETASGRVVALRPLKRGGLGIIIPSSIGELDLHRYLDLSGNSLVGVPKSLQIRLK 123

Db 61 WEIAC-GSGVTTELSSFMALLEGPIVSIAWLTGLRLDLSSLSGELPEL---IS 116
QY 124 SLTDSQSGLMGSIINMLLVSSRTTIDEEPNTISGTNNVSGG--SNNVSGNDNTVVS 180
Db 117 SASVAFDVSNFNLGELQESS-PSLPHPLOVLNLSHFFPAGEFPSTWEEKSDLVAIN 175
QY 181 GNNHVSGSNNVTVTGSDNTVSGNHVSGTKHIVTD-NNNVSGNDNNVSGSFHTVSGE 239
Db 176 ASHTPESG-----LPSSFCISSPSPAVLDLSYNFLSGSIPAEIGKCSL--- 220
QY 240 HNTVSGSNNVTSGS 253
Db 221 -RVLKASNNNEINGS 233

RESULT 5

US-10-437-963-172660
; Sequence 172660, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172660
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70775C.1.pap
US-10-437-963-172660

Query Match 14.2%; Score 197; DB 16; Length 961;
Best Local Similarity 29.5%; Pred. No. 4e-08;
Matches 82; Conservative 38; Mismatches 102; Indels 56; Gaps 15;

QY 10 MLLVFLGFILOVAGATWS-CHDDHLALRGLAENLSGKAVRLRAWSGAS--CCSWEG 66
Db 4 MOWLLLFLLVSLRLSFSQTPNQDYSALQALMKWQNE-----PQSMWGSTDPCTSDG 58
QY 67 VGCETASGRVVALRLPKRGIGGIIPSSIGELDLRLYLDLSGN-SLVGEVPKSLQIRLKS 125
Db 59 ISC-SNGRVTMRLSGINLQGLTSLNAIDQLSLTYLDLSNNLNGPLPPSI-VNLKQL 115
QY 126 TT-----DSQSLGMSGINMLLVSSRT-----LDEEPNTISG 158
Db 116 TTLILGCSFTGDIPEQIGALRLTLALNSKNFTGGIPPTLGLSKLFWLDLSDNQLSG 175
QY 159 TNNVSGSNNVSGNDNTVSGNNHVSGSNNVTVTGSDNTVSGNHVSGTKHIVTDN 218
Db 176 -KIPVSGSN---PGLDQLV---NAEHFFHSENLGTGPIDEKLFSEK---MNLHIVFDN 225
QY 219 NNV---VSGNDNNVSGSFHTVSGEHTVSGSNNVTSGS 253
Db 226 NNTGPIGSLGRVS-SIQIRLDHRNQFSQ---PVPGS 259

RESULT 6

US-10-437-963-115627
; Sequence 115627, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 115627
; LENGTH: 917
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_19205C.1.pap
US-10-437-963-115627

Query Match 14.0%; Score 194; DB 16; Length 917;
Best Local Similarity 26.3%; Pred. No. 6.8e-08;
Matches 81; Conservative 43; Mismatches 108; Indels 76; Gaps 12;

QY 6 AKCCMLLVFLGFILOVAGATWSCHDDHLALRGLAENLSGKAVRLRAWS--GASCCS 63
Db 4 ATAAULLLTAAILAAAGAV-----NDQVLAIVVFKSGVSDPGGV--LAAMSEADADRA 56
QY 64 WEGVCGETASGRVVALRLPKRGIGGIIP-SSIGELDLRLYLDLSGNLSVGEVPKSLQIRL 122
Db 57 WPGVSCDARAGRVDVALPFSAGLSGRLPRSAALLRLDALLSLALPGNLSGPLPDALPPRA 116
QY 123 KSLTTDSQSL-----GMGSINM-----LLHYSSRRTLDDEPNTISG 158
Db 117 RALDLSANSLSGYLPAALASCSSLSLNSLNSLNSLNSLNSLNSLNSLNSLNSLNSL 176
QY 159 TNNVSGG-----SNNVSGNDNTVVS-----GNNHVSGSNNVT--V 194
Db 177 ---SVPGGFPRSSLRVLDLSRLNLEGEIPADVGEAGLLKSLDVGHNLFTGELPESL 233
QY 195 TGSDNTVVGSNHV-----VSGTKHIVTDNNNVSGNDNNVSGSFHTVSGEHTVVS 244
Db 234 TGLSLGAGGNALAGELPGWIGEMAALETLDLSGNRFVGAIPDGISGCKNLVE-----VD 288
QY 245 GSNNTVSG 252
Db 289 LSGNALTG 296

RESULT 7

US-10-437-963-192784
; Sequence 192784, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 192784
; LENGTH: 1164
; TYPE: PRT

Qy	127	TDSOSLGWGSINMLLHVSRRLTDEEPTNISGTNNVSGSNN-----VVSGNDNTVVS	180
Dz	346	-----IFSGSIIV-----LDVSNRLGGEIQEVDSSTDWPLOVLNITSSNLFTGAF	391
Qy	181	GNNNHVSGSNVTVTGSDNTVVG---SNHVSVGTKHIVTD-----NNNVVSG-----	224
Dz	392	PSTTWKMSNLVAINGSNNSPTGHIPSGFCISLSFAALDLCYNQFSGEIPAGIKCSAL	451
Qy	225	-----NNNVVSGS-----FHTVSGEHNTVSGSNNTVSGS--NHIVSGSKNVTD	266
Dz	452	RMLKAGHNITSGLAPDLDFIATSLSEY--LSPPNNGLOQTIKLVKLSNLVFD	502

RESULT 9
US-10-437-963-153194
; Sequence 153194, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with Rice
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204965

```

? LENGTH: 1060
? TYPE: PRT
? ORGANISM: Oryza sativa
? FEATURE:
? OTHER INFORMATION: Clone ID: PAT_MRT4530_53170C.1.pep
US-10-437-963-153194

Query Match 13.9%; Score 192; DB 16; Length 1060;
Best Local Similarity 27.5%; Pred. No. 1.2e-07;
Matches 72; Conservative 44; Mismatches 112; Indels 34; Gaps 9;

QY 11 LLVFLGFIQVAGATSWCHDDDLHALRGLAENL-----SGKGAVRLRAAWSGASCC 62

```

```

QY      226  DNVSG--SPTVSGEHTVSG 245
      :| | | | :| |
      :| | | | :| |
Db      245  PDDVFGLTSLQVLSLHTNSLSG 266

RESULT 10
US-10-437-963-162505
; Sequence 162505, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

```

APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 162505
LENGTH: 1044
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_61590C.1.p
US-10-437-963-162505

Query Match 13.7%; Score 190; DB 16; Length 1044;
Best Local Similarity 26.5%; Pred. No. 1.8e-07;
Matches 79; Conservative 47; Mismatches 114; Indels 58; Gaps 14;

QY 1 MPEYMAKCCMLLVFLG-FILOVAGATSWCHHD-DLHALRGLAENLSG-KGAVRLRAAWS 57
DB 1 MIRLFASCPKLIPLAVFIFFSSSLPLAISDDTDTREALLCFKQISDPNGAL---SSWT 57
QY 58 GASC--CSWEGVCETASG--RVVALRKPRLGGIIPSSIGELDLRLYLDLGSNSLVGE 113
DB 58 NTSLNFCWQGVSCNTPQPLRVMLNVSQKGLGGLIPPCIGNLSSIASLSDLSNNAFLGK 117
QY 114 VPKSL---QIRLKSITTDQSGLMGSIINMLL-HVSSRRRLDEPNTISGTNNVSGSG-- 166
DB 118 IPSELGHLQISVNL-----SINSLGHIPELSCSKLKVLSLKNLSLQGEIP 167
QY 167 -----SNNVSGNDNT-----VSGNNHVSNNVTVTGSDNTV-- 201
DB 168 PSITQCTHLQVVLNCKNLQGRIPKFGMLHEKLTLDLSNNALTGDIPLLAGSSPSFVVV 227
QY 202 -VGSNNHVSCTKHIVTDNN--VSGNDNNVSGSFHTV---SGEHTVSGNNVTVSGS 253
DB 228 DLGGNQLTGGIPEFLANSSSLQVLSLKQNNLTGIPPSIFNSSKLTIIYLRNNLVGS 285

RESULT 11
US-10-437-963-172329
; Sequence 172329, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172329
; LENGTH: 1011
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70476C.1.p
US-10-437-963-172329

Query Match 13.6%; Score 188.5; DB 16; Length 1011;
Best Local Similarity 30.5%; Pred. No. 2.3e-07;

Matches 74; Conservative 32; Mismatches 88; Indels 49; Gaps 12;
QY 11 LLVFLGFILQVAGATSWCHHD-DLHALRGLAENLSGKAVR-----LRAAWSGAS----- 60
DB 4 MLSLLTHALLQTIVTSQTGGDLSAL-----LSFKSLIRDDPREVMSWDTAGNTNM 57
QY 61 ----CCSWEGVCETA--SGRVVALRKPRLGGIIPSSIGELDLRLYLDLGSNSLVGEV 114
DB 58 PAPVICQMTGVSNNRRHPRVTTLRLSGAGLVGTISPOLGNLTHLRVLDLSANSLDGOI 117
QY 115 PKSL---QIRLKSITTDQSGLMGSIINMLLHVSSRRRLDEPNTISGTNNVSGSGNNV 170
DB 118 PASLGGCRKRLTNLJNLSHLS---GSIPLDGLGSSKLAIFD-----VGHNNLTGVPKSP 169
QY 171 VSGNDNTVVSNNHVSNNVTVTGSDNTVVSNNHVSCTKHIVTDNNNVSGNDNNVS 230
DB 170 --SNLTTLV---KPIETN--PIDGKDLNMGNN---LTSLTHFVLEGNRFT---GNIP 214
QY 231 GSF 233
DB 215 ESF 217

RESULT 12
US-10-437-963-123119
; Sequence 123119, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 123119
; LENGTH: 1078
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1078)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_25984C.1.p
US-10-437-963-123119

Query Match 13.6%; Score 188.5; DB 16; Length 1078;
Best Local Similarity 28.5%; Pred. No. 2.5e-07;
Matches 76; Conservative 32; Mismatches 92; Indels 67; Gaps 12;
QY 12 LVFLGFILQVAGAT-----SWSCHDDLHALRGLAENLSGKAVRLRAAWSGA-SCCSWEG 66
DB 8 VVSGVLVLVLAATTCGRAACAERAAALSLAEASPPAGDAIVADWRGSPDCCRWDG 67
QY 67 VGCETA---SGRVVALRKPRLGGIIPSSIGELDLRLYLDLGSNSLVGVRPK----- 116
DB 68 VCGGAGDGDGAVTRLSLGRGFNGTISFGNLTGLTHNLNSGSLAGOFFEVLPSLPN 127
QY 117 -----SLQIRLKSITTDQSGLMGSIINMLLHVSSRRRLDEPNTI-----S 157
DB 128 VTVDVSVNCLSGELPSVATGAAGGLSLE-VLDVSSNLLAGQFPFSAIWEHTPRLVSLN 186
QY 158 GTNNVSGSG-----SNNVSGNDNTVVS---GNNHVV-----SGSNNTVV 194
DB 187 ASNNSPHGSIPSLCVSCPALAVLDLSNVVLSG----VISPGFGNCSQLRVLISGRNN--L 240

QY 195 TGSNDTVGSGNHVSGTGHVTDNNV 221
||| :||| :
Db 241 TGE---LPGLFDVKALQHLPLPANI 264

RESULT 13

US-10-424-599-267766
; Sequence 267766, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 267766
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(278)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_83815C.1.pap
US-10-424-599-267766

Query Match 13.4%; Score 186; DB 15; Length 278;
Best Local Similarity 30.3%; Pred. No. 7.2e-08;
Matches 71; Conservative 23; Mismatches 70; Indels 70; Gaps 10;

QY 1 MPEYMAKCMMLVFLGFILOVAGATWSCHDDHLHALR-GIAENLSGKAVRLRAWSG-- 58
||| :||| :
Db 1 MKSARVKEAILLVFMSLSIA-----C--SDLASDRA-----GLLLRSVAGRT 44
QY 59 -----ASCSWGVGCTASGRVVALRPLKGLGIIIP-SSIGELDHRLYLDLNSLV 111
Db 45 LLWNSTQSPCSWTGVGC--ASGRVIMLRPLAMGLSGSLPSGLNLTQLTLRFLNALT 102
QY 112 GEVPSLQIRLKSLL-----TTDS-----QSLGMSINMLLHVSR----- 146
Db 103 GRIPEDF-ANLKSRLNLYLQGNFFSGVSDSVFALQNLVRLNNGNPFSGEISPKFNSLT 161
QY 147 --RTLDEPNTISG-----TNNVSGSGNNVYVSGNDNTVVGSGNN 183
Db 162 RLATLYLERNNFTGSIPLDAPPLDQFNVSFNSLTGSIPIKFRSLDRDTAPLGN 215

RESULT 14

US-10-437-963-153306
; Sequence 153306, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 153306
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(676)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_53274C.1.pap
US-10-437-963-153306

Query Match 13.4%; Score 186; DB 16; Length 676;
Best Local Similarity 30.4%; Pred. No. 2.3e-07;
Matches 70; Conservative 30; Mismatches 98; Indels 32; Gaps 8;

QY 1 MPEYMAKCMMLVFLGFILOVAGATWSCHDDHLHALR-GIAENLSGKAVRLRAWSGA 59
||| :||| :
Db 1 MPPRLPCLAAFLALALVWVCA-----EPDADRAALLDFLAGLGGGRINWASS 52
QY 60 S--CCSWGVGCTASGRVVALRPLKGLGIIIP-SSIGELDHRLYLDLNSLVGEVPSK 116
||| :||| :
Db 53 PRVCGNWTGVTCSGDGSRVVALRPLGLSGPVRGTIGRLTALQVLSLRANSLSGEPPE 112
QY 117 SLQIRLKSLLTDSQSGLMGSGINM---LLHVSSRRTLDEEPNTISGTNNVSGSGNNVVG 173
||| :||| :
Db 113 EL-LSLASLTGLHLQNAFSGALPPELRLARLQVLDLSPNGFNGTLPALSLNLTQVAL 171
QY 174 N-DNTVVVG-----NNHVSGSGNNVTVTGSNDTVVGSGNHV 207
||| :||| :
Db 172 NLSNNSLSGRVPDLGALPALQFLNLSNNHLDGPVPTSLRFDNTAFAGNV 221

RESULT 15

US-10-437-963-192786
; Sequence 192786, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 192786
; LENGTH: 1012
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_88985C.1.pap
US-10-437-963-192786

Query Match 13.4%; Score 185; DB 16; Length 1012;
Best Local Similarity 25.6%; Pred. No. 4.6e-07;
Matches 87; Conservative 35; Mismatches 116; Indels 102; Gaps 12;

QY 8 CCMMLVFLGFILOVAGATWS--CHDDHLHALRGLAENLSGKAVRLRAWSGSCCSWE 65
||| :||| :
Db 6 CFHFPLVSVLLVHVHGRSESCQDPTDLAALLAFSDGLDTKAAGVMVWGPGDAACCSWT 65
QY 66 GVCCTASGRVVALRPLKGL-----GGIIPSSIGELDHRLYLDLNSLVGEVPSKSLQ 119
||| :||| :
Db 66 GVSCDL--GRVVALDLSNLSRNSLRGGEAVARGLRSLRLDLSANGLAFAFPAG-- 121
QY 120 IRLKSLTTDSQSGLMGSGINMLHVSSRRTLDEEPNTISGTNNVSGSGNNVSGNDNT-- 177

```
Db 122 -----GFAIE-VNVSSNGFTGPHAFPGAPNLTVDITGNAPSGGINVTA 167
Qy 178 -----VMSGNNHVSQS-----NNTVVVTS----- 197
Db 168 LCASPVKVLRFSANAFSGDVPAGFGOCKLLNDLFLDGNGLTGS LPKDLYMMPALRKLSQLQ 227
Qy 198 DNTVGSNNHVSQTKHIVTD---NNNVSGNDNNVSG-----SFHTVSGEHN----- 241
Db 228 ENKLSGLDDDLGNLTETITQIDLSYNNFNGNIPDVEFKLRSLESNLASNLQNLGTLPLSL 287
Qy 242 -----TVSGSNNTVSGS-----NHIVSGSNKV 263
Db 288 SSCFMRLRVVSLRNNLSGEITIDCRLLTRLNPFDA GTNKL 327
```

Search completed: May 9, 2005, 20:34:42
Job time : 144 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2005, 20:10:27 ; Search time 73 Seconds
(without alignments)
1414.589 Million cell updates/sec

Title: US-10-657-852a-15

Perfect score: 1385

Sequence: 1 MPEYAKCCMLLVFLGLFIQL.....NTVSGSNHIVGSKNVKVTID 267

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Genesecp1980s:*

2: Genesecp1990s:*

3: Genesecp2000s:*

4: Genesecp2001s:*

5: Genesecp2002s:*

6: Genesecp2003as:*

7: Genesecp2003bs:*

8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1385	100.0	267	8	Adm41473 Perennial
2	1290	93.1	269	8	Adm41474 Tall fesc
3	992.5	71.7	262	8	Adm41481 Tall fesc
4	980.5	70.8	254	8	Adm41480 Perennial
5	973.5	70.3	256	8	Adm41482 Perennial
6	910.5	65.7	277	8	Adm41477 Perennial
7	908.5	65.6	277	8	Adm41476 Tall fesc
8	904.5	65.3	281	8	Adm41483 Perennial
9	901.5	65.1	281	8	Adm41475 Perennial
10	901.5	65.1	285	8	Adm41479 Tall fesc
11	884	63.8	280	8	Adm41478 Perennial
12	668	48.2	243	8	Adm41472 Tall fesc
13	655	47.3	243	8	Adm41471 Perennial
14	530	38.3	118	2	Aay22472 Grass ant
15	258.5	18.7	1036	5	Abb93804 Herbicide
16	204	14.7	1021	8	Adoi4158 Carrot ph
17	197.5	14.3	598	3	Aag20654 Arabidops
18	197.5	14.3	599	3	Aag20653 Arabidops
19	197.5	14.3	751	5	Abb93984 Herbicide
20	190.5	13.8	1008	8	Adn72587 Thale cre
21	182	13.1	941	2	Aaw68205 M. catarr
22	181	13.1	653	8	Adj49621 Oll-absoc
23	177	12.8	892	2	Aaw68203 M. catarr
24	176.5	12.7	735	3	Aag32217 Arabidops
25	176.5	12.7	743	3	Aag32216 Arabidops

26	176.5	12.7	804	3	AAB25515	Aab25515 Pinus rad
27	176	12.7	852	6	ABU34968	Abu34968 Protein e
28	175	12.6	889	2	AAW68208	Aaw68208 M. catarr
29	174	12.6	843	3	AAB25518	Aab25518 Pinus rad
30	173.5	12.5	590	5	ABB91206	Abb91206 Herbicide
31	171.5	12.4	323	3	AAB25445	Aab25445 Pinus rad
32	170.5	12.3	386	3	AAB25527	Aab25527 Pinus rad
33	170.5	12.3	707	3	AAB25112	Aab25112 Pinus rad
34	170	12.3	624	2	AAW68204	Aaw68204 M. catarr
35	168.5	12.2	187	3	AAB25413	Aab25413 Pinus rad
36	168.5	12.2	1095	5	ABB91562	Abb91562 Herbicide
37	166.5	12.0	938	8	ADQ36979	Adq36979 Cell prol
38	166.5	12.0	938	8	ADQ15649	Adq15649 Rice stre
39	166	12.0	966	5	ABB93915	Abb93915 Herbicide
40	166	12.0	966	8	ADI32622	Adi32622 Thale cre
41	165.5	11.9	854	4	AAW42228	Aaw42228 Soybean r
42	165.5	11.9	854	4	AAW42230	Aaw42230 Soybean r
43	165.5	11.9	854	4	AAW42232	Aaw42232 Soybean r
44	165	11.9	627	5	ABB92188	Abb92188 Herbicide
45	165	11.9	627	8	ADN72847	Adn72847 Thale cre

ALIGNMENTS

RESULT 1

ADM41473

ID ADM41473 standard; protein; 267 AA.

XX ADM41473;

DT 03-JUN-2004 (first entry)

DE Perennial ryegrass antifreeze protein AFP2.

XX Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;

KW antitout; litholytic; nephrotropic; cytotostatic.

OS Lolium perenne.

XX Key Location/Qualifiers

FT Peptide 1..23

FT Region /label= Signal_peptide

FT Region 60..71 /note= "Conserved Cys pairs identified N-terminal of

FT Region /note= "Conserved leucine-rich repeats of receptor-like kinases"

FT Region 76..117 /note= "Conserved leucine-rich repeats"

FT Region 152..266 /note= "7-amino acid sequence repeat region identified in

FT Region antifreeze proteins"

WO2004022700-A2.

18-MAR-2004.

09-SEP-2003; 2003WO-NZ000199.

09-SEP-2002; 2002US-0409557P.

(GENE-) GENESIS RES & DEV CORP LTD.

(WRIG-) WRIGHTSON SEEDS LTD.

Demmer D) Shenk WA, Hall C, Fish SA;

WPI; 2004-248453/23.

N-PSDB; ADM41460.

New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted biocrystals (e.g. gout).

PS Claim 7; SEQ ID NO 16; 71pp; English.

XX The present sequence is that of APP2, an antifreeze protein of perennial

CC ryegrass. The encoding cDNA was isolated from a leaf blade cDNA

CC expression library. The invention provides forage grass (perennial

CC ryegrass and tall fescue) antifreeze proteins and the polynucleotides

CC encoding them ADM41458-ADM41483. The polynucleotides were isolated from

CC tissues taken at different times of year (winter and spring) and from

CC different parts of the plants. The polynucleotides can be used to

CC modulate the cold tolerance of an organism, especially plants, mammals,

CC insects, fungi, archaea and bacteria. The method involves incorporating

CC an antifreeze polynucleotide, under the control of a gene promoter

CC sequence, into the genome of the organism, or introducing double-stranded

CC RNA corresponding to the polynucleotide into the cells of the organism,

CC thereby inhibiting expression of an antifreeze polypeptide. The

CC antifreeze protein can be used for the cryopreservation of a cell or

CC tissue, as a food additive of a frozen food product, in a method for

CC decreasing the time required to dehydrate a composition, to treat a

CC disorder characterised by biocrystals associated with disorders such as

CC gout and kidney stones, to preserve the viability of a molecular biology

CC reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and

CC to protect a plant from damage due to frost or freezing.

XX Sequence 267 AA;

Query Match 100.0%; Score 1385; DB 8; Length 267;

Best Local Similarity 100.0%; Pred. No. 5.4e-114;

Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPEYMAKCMMLVFLGFILOVAGATSWSCHDDDLHALRGLAENLSGKGAVALRAAWSGAS 60

DB 1 MPEYMAKCMMLVFLGFILOVAGATSWSCHDDDLHALRGLAENLSGKGAVALRAAWSGAS 60

QY 61 CCSWEGVGCETASGRVVALRPLPKRGLGIIIPSSIGELDHLYLDLGSNLSVGEVPSKLSQI 120

DB 61 CCSWEGVGCETASGRVVALRPLPKRGLGIIIPSSIGELDHLYLDLGSNLSVGEVPSKLSQI 120

QY 121 RLKSLTTDSQSLGMSINMLLHVSSRRRLDDEPNTISGTNNVSGSNVSGNDNTVVS 180

DB 121 RLKSLTTDSQSLGMSINMLLHVSSRRRLDDEPNTISGTNNVSGSNVSGNDNTVVS 180

QY 181 GNNNHVSGSNNTVVTGSDNTVVGSNHVSFGTKHIVTDNNNVSGNDNNVSGSFHTVSGEH 240

DB 181 GNNNHVSGSNNTVVTGSDNTVVGSNHVSFGTKHIVTDNNNVSGNDNNVSGSFHTVSGEH 240

QY 241 NTVSGSNNTVSGSNHIVSGSNKVVTDG 267

DB 241 NTVSGSNNTVSGSNHIVSGSNKVVTDG 267

RESULT 2

ADM41474

ID ADM41474 standard; protein; 269 AA.

XX AC ADM41474;

XX DT 03-JUN-2004 (first entry)

XX DE Tall fescue antifreeze protein.

XX KW Antifreeze; fescue; cold tolerance; transgenic; plant; antitout;

XX KW litholytic; nephrotropic; cytostatic.

XX OS Schedonorus arundinaceus.

XX FH Key Location/Qualifiers

FT Peptide 1..24

FT /label= signal_peptide

FT Region 61..72

FT /note= "Conserved Cys pairs identified N-terminal of

FT leucine-rich repeats of receptor-like kinases"

FT 77..118

FT /note= "Conserved leucine-rich repeats"

FT Misc-difference 124

FT /note= "Encoded by TAG"

FT Region 154..268

FT /note= "7-amino acid sequence repeat region identified in

FT antifreeze proteins"

PN WO2004022700-A2.

XX 18-MAR-2004.

XX 09-SEP-2003; 2003WO-NZ000199.

XX 09-SEP-2002; 2002US-0409557P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (WRIG-) WRIGHTSON SEEDS LTD.

XX Demmer J, Shenk MA, Hall C, Fish SA;

XX WPI; 2004-248453/23.

XX N-PSDB; ADM41461.

XX New antifreeze proteins and encoding polynucleotides, useful for

XX modulating cold tolerance in organisms, as food additives, or for

XX treating tumors or disorders associated with the presence of unwanted

XX biocrystals (e.g. gout).

XX Claim 7; SEQ ID NO 17; 71pp; English.

The present sequence is that of an antifreeze protein of tall fescue. The

encoding cDNA was isolated from a leaf blade cDNA expression library. The

invention provides forage grass (perennial ryegrass and tall fescue)

antifreeze proteins and the polynucleotides encoding them ADM41458-

ADM41483. The polynucleotides were isolated from tissues taken at

different times of year (winter and spring) and from different parts of

the plants. The polynucleotides can be used to modulate the cold

tolerance of an organism, especially plants, mammals, insects, fungi,

archaea and bacteria. The method involves incorporating an antifreeze

polynucleotide, under the control of a gene promoter sequence, into the

genome of the organism, or introducing double-stranded RNA corresponding

to the polynucleotide into the cells of the organism, thereby inhibiting

expression of an antifreeze polypeptide. The antifreeze protein can be

used for the cryopreservation of a cell or tissue, as a food additive of

a frozen food product, in a method for decreasing the time required to

dehydrate a composition, to treat a disorder characterised by biocrystals

associated with disorders such as gout and kidney stones, to preserve the

viability of a molecular biology reagent, to destroy unwanted tissue in a

patient e.g. tumour tissue, and to protect a plant from damage due to

frost or freezing.

XX Sequence 269 AA;

Query Match 93.1%; Score 1290; DB 8; Length 269;

Best Local Similarity 93.3%; Pred. No. 1.4e-105;

Matches 251; Conservative 6; Mismatches 10; Indels 2; Gaps 2;

QY 1 MPEYMAKCMMLVFLGFI-LOVAGATSWSCHDDDLHALRGLAENLSGKGAVALRAAWSGA 59

DB 1 MPEYMAKCMMLLALLAFILLOVAGATSWSCHDDDLRALRGLFAENLSGKGAVALRAAWSGA 60

QY 60 SCCSWEGVGCETASGRVVALRPLPKRGLGIIIPSSIGELDHLYLDLGSNLSVGEVPSKLSQ 119

DB 61 SCCSWEGVGCETASGRVVALRPLPKRGLGIIIPSSIGELDHLYLDLGSNLSVGEVPSKLSQ 120

QY 120 IRLKSLTTDSQSLGMSINMLLHVSS-RRYLDDEPNTISGTNNVSGSNVSGNDNTV 178

DB 121 IRLKSLTTDSQSLGMSINMLLHVSSRRYLDDEPNTISGTNNVSGSNVSGNDNTV 180

QY 179 VSGNNNHVSGSNNTVVTGSDNTVVGSNHVSFGTKHIVTDNNNVSGNDNNVSGSFHTVSG 238

DB 181 ISGNNNHVSGSNNTVVTGSDNTVVGSNHVSFGTKHIVTDNNNVSGNDNNVSGSFHTVSG 240

QY 239 EHNTVSGSNNTVSGSNHIVSGSNKVVTDG 267

New antifreeze proteins and encoding polynucleotides, useful for

PT modulating cold tolerance in organisms, as food additives, or for
 PT treating tumors or disorders associated with the presence of unwanted
 PT biocrystals (e.g. gout).

PS Claim 7; SEQ ID NO 23; 71pp; English.

XX The present sequence is that of APP5, an antifreeze protein of perennial
 CC ryegrass. The encoding cDNA was isolated from a leaf blade cDNA
 CC expression library. The invention provides forage grass (perennial
 CC ryegrass and tall fescue) antifreeze proteins and the polynucleotides
 CC encoding them ADM41458-ADM41483. The polynucleotides were isolated from
 CC tissues taken at different times of year (winter and spring) and from
 CC different parts of the plants. The polynucleotides can be used to
 CC modulate the cold tolerance of an organism, especially plants, mammals,
 CC insects, fungi, archaea and bacteria. The method involves incorporating
 CC an antifreeze polynucleotide, under the control of a gene promoter
 CC sequence, into the genome of the organism, or introducing double-stranded
 CC RNA corresponding to the polynucleotide into the cells of the organism,
 CC thereby inhibiting expression of an antifreeze polypeptide. The
 CC antifreeze protein can be used for the cryopreservation of a cell or
 CC tissue, as a food additive of a frozen food product, in a method for
 CC decreasing the time required to dehydrate a composition, to treat a
 CC disorder characterised by biocrystals associated with disorders such as
 CC gout and kidney stones, to preserve the viability of a molecular biology
 CC reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
 CC to protect a plant from damage due to frost or freezing.

XX Sequence 254 AA;

Query Match 70.8%; Score 980.5; DB 8; Length 254;
 Best Local Similarity 73.5%; Pred. No. 3e-78;
 Matches 194; Conservative 24; Mismatches 33; Indels 13; Gaps 3;
 QY 5 MAKCCMLLVFLGFILOVAG-AFTWSCHDDHLALRGLAENISGKAVRLRAAWSGSCCS 63
 DB 1 MAKCLMLLLSFAFLSAGTATATPCHRDDLALRGLAENISGKAVRLRAAWSGSCCD 60
 QY 64 WEGVGCETASGRVVALRPLKRGIGIIPSSIGELDLRLYLDSGNSLVGEVPKSLQIRLK 123
 DB 61 WEGVGCDCGASGRVTALWLPRLSGLTGPIPSWICQLHLRLYLDSGNSLVGEVPKLQVQK 120
 QY 124 SLTTDSQSLGMSINMLLHV-SSRRTLDEEPTISGTNNVSGSGNNVSGNDNTVSGN 182
 DB 121 GIT-----NPLHVMNRSLDEQPTISGNNVSGSKVLAGNDNTVIGSD 169
 QY 183 NNVSGSNNVTGSDNTVGSNNHVSGTKHIVTDNNNVSGNDNNVSGSFHTVSGHNT 242
 DB 170 NNVSGSNNVTGSDNTVGSNNHVSGTNHIVTDNNNVSGNDNNVSGSFHTVSGGHT 229
 QY 243 VSGSNNVTGSGNHVSGSKVVTVD 266
 DB 230 VSGSNNVTGSGNHVSGSKVVTVD 253

RESULT 5

ADM41482
 ID ADM41482 standard; protein; 256 AA.

XX ADM41482;

DT 03-JUN-2004 (first entry)

XX Perennial ryegrass antifreeze protein.

XX Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;

KW antitout; litholytic; nephrotropic; cytostatic.

XX Lolium perenne.

XX Key Location/Qualifiers

FT Peptide 1..23

FT /label= signal_peptide

FT Region 59..70

FT /note="Conserved Cys-pairs identified N-terminal or
 FT leucine-rich repeats of receptor-like kinases"
 FT 75..116
 FT /note="Conserved leucine-rich repeats"
 FT 141..255
 FT /note="7-amino acid sequence repeat region identified in
 FT antifreeze proteins"

XX W02004022700-A2.

PN 18-MAR-2004.

XX 09-SEP-2003; 2003WO-NZ000199.

XX 09-SEP-2002; 2002US-0409557P.

XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA (WRIG-) WRIGHTSON SEEDS LTD.

XX Demmer J, Shenk MA, Hall C, Fish SA;

XX WPI; 2004-248453/23.

DR N-PSDB; ADM41469.

XX New antifreeze proteins and encoding polynucleotides, useful for
 PT modulating cold tolerance in organisms, as food additives, or for
 PT treating tumors or disorders associated with the presence of unwanted
 PT biocrystals (e.g. gout).

XX Claim 7; SEQ ID NO 25; 71pp; English.

PS The present sequence is that of an antifreeze protein of perennial
 CC ryegrass. The encoding cDNA was isolated from a leaf and pseudostem cDNA
 CC expression library. The invention provides forage grass (perennial
 CC ryegrass and tall fescue) antifreeze proteins and the polynucleotides
 CC encoding them ADM41458-ADM41483. The polynucleotides were isolated from
 CC tissues taken at different times of year (winter and spring) and from
 CC different parts of the plants. The polynucleotides can be used to
 CC modulate the cold tolerance of an organism, especially plants, mammals,
 CC insects, fungi, archaea and bacteria. The method involves incorporating
 CC an antifreeze polynucleotide, under the control of a gene promoter
 CC sequence, into the genome of the organism, or introducing double-stranded
 CC RNA corresponding to the polynucleotide into the cells of the organism,
 CC thereby inhibiting expression of an antifreeze polypeptide. The
 CC antifreeze protein can be used for the cryopreservation of a cell or
 CC tissue, as a food additive of a frozen food product, in a method for
 CC decreasing the time required to dehydrate a composition, to treat a
 CC disorder characterised by biocrystals associated with disorders such as
 CC gout and kidney stones, to preserve the viability of a molecular biology
 CC reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
 CC to protect a plant from damage due to frost or freezing.

XX Sequence 256 AA;

Query Match 70.3%; Score 973.5; DB 8; Length 256;
 Best Local Similarity 72.6%; Pred. No. 1.3e-77;
 Matches 193; Conservative 24; Mismatches 34; Indels 15; Gaps 3;

QY 5 MAKCCMLLVFLGFILOVAG---ATWSCHDDHLALRGLAENISGKAVRLRAAWSGASC 61

DB 1 MAKCLMLLLSFAFLSAGTATATPCHRDDLALRGLAENISGKAVRLRAAWSGASC 60

QY 62 CSWEGVGCETASGRVVALRPLKRGIGIIPSSIGELDLRLYLDSGNSLVGEVPKSLQIR 121

DB 61 CDWEGVGCDCGASGRVTALWLPRLSGLTGPIPSWIFQLHLRLYLDSGNSLVGEVPKLQVQ 120

QY 122 LKSLTTDSQSLGMSINMLLHV-SSRRTLDEEPTISGTNNVSGSGNNVSGNDNTVVS 180

DB 121 LKGIT-----NPLHVMNRSLDEQPTISGNNVSGSKVLAGNDNTVIS 169

QY 181 GNNHVSGSNNVTGSDNTVGSNNHVSGTKHIVTDNNNVSGNDNNVSGSFHTVSGEH 240

DB 170 GDNVSGSNNVTGSDNTVGSNNHVSGTNHIVTDNNNVSGNDNNVSGSFHTVSGGH 229

The present sequence is that of AFP3, an antifreeze protein of perennial ryegrass. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them (ADMA1458-ADMA14483). The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a

DR N-PSDB; ADM41463.

XX New antifreeze proteins and encoding polynucleotides, useful for

PT modulating cold tolerance in organisms, as food additives, or for

FT treating tumors or disorders associated with the presence of unwanted

PT biocrystals (e.g. gout).

XX

PS Claim 7; SEQ ID NO 19; 71pp; English.

XX

XX The present sequence is that of an antifreeze protein of tall fescue. The

CC invention provides forage grass (perennial ryegrass and tall fescue). The

CC antifreeze proteins and the polynucleotides encoding them ADM41458-

CC ADM41483. The polynucleotides were isolated from tissues taken at

CC different times of year (winter and spring) and from different parts of

CC the plants. The polynucleotides can be used to modulate the cold

CC tolerance of an organism, especially plants, mammals, insects, fungi,

CC archaea and bacteria. The method involves incorporating an antifreeze

CC polynucleotide, under the control of a gene promoter sequence, into the

CC genome of the organism, or introducing double-stranded RNA corresponding

CC to the polynucleotide into the cells of the organism, thereby inhibiting

CC expression of an antifreeze polypeptide. The antifreeze protein can be

CC used for the cryopreservation of a cell or tissue, as a food additive of

CC a frozen food product, in a method for decreasing the time required to

CC dehydrate a composition, to treat a disorder characterised by biocrystals

CC associated with disorders such as gout and kidney stones, to preserve the

CC viability of a molecular biology reagent, to destroy unwanted tissue in a

CC patient e.g. tumour tissue, and to protect a plant from damage due to

CC frost or freezing.

XX

XX Sequence 277 AA;

Query Match 65.6%; Score 908.5; DB 8; Length 277;

Best Local Similarity 67.9%; Pred. No. 86-72; Mismatches 19; Gaps 4;

Matches 188; Conservative 19; Indels 19; Gaps 4;

QY 5 MAKCCMLLVFLGFIQVAGATSWCHDDHLAGRLAENLSCGKAVRLRAAGSCCSCW 64

DB 1 MAKCCMLLVFLVLLPAAAT--SCHPDDLRLRGFVGNLNG--GGVLLHGAWSGLCCAW 57

QY 65 EGVGCETASGRVVALRLP-----KRLGGIIPSSIGELDLHRLYDLDSNS 109

DB 58 EGVGCETASGRVVALRLPISLEDCGKLSINLANERLVGTIPSWIGELDHCHVILSDNS 117

QY 110 LVGEVPSLQIRKSLITDSQSLMGSIINMLHV--SSRRTLDEPNTTSGTNNVSGGSSN 168

DB 118 LVGKVPNSLQIRKSLITDSQSLMGSIINMLHV--SSRRTLDEPNTTSGTNNVSGGSSN 177

QY 169 NVVSGNDNTVSGNNHVSNNVSGNNVTGSDNTVSGSNHVSCTKHIVTDNNNVSGNDNN 228

DB 178 NAVSGNDNTVSGNNHVSNNVSGNNVTGSDNTVSGSNHVSCTKHIVTDNNNVSGNDNN 237

QY 229 VSGSPHTVSGHNTVSGNNVTGSDNTVSGSNHVSCTKHIVTDNNNVSGNDNN 265

DB 238 VSGSHTVSGHNTVSGNNVTGSDNTVSGSNHVSCTKHIVTDNNNVSGNDNN 274

RESULT 8

ADM41483

ID ADM41483 standard; protein; 281 AA.

XX

AC ADM41483;

XX

DT 03-JUN-2004 (first entry)

XX

DE Perennial ryegrass antifreeze protein.

XX

XX Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;

KW antigout; litholytic; nephrotropic; cytostatic.

XX

OS Lolium perenne.

XX

XX Key Location/Qualifiers

FT Peptide 1..19

FT Region /label= Signal_peptide

FT 10..22

FT /note= "Conserved lipoprotein membrane attachment site"

FT 53..64

FT /note= "Conserved Cys-pairs identified N-terminal or

FT leucine-rich repeats of receptor-like kinases"

FT 69..125

FT /note= "Conserved leucine-rich repeats"

FT 165..279

FT /note= "7-amino acid sequence repeat region identified in

FT antifreeze proteins"

WO2004022700-A2.

18-MAR-2004.

09-SEP-2003; 2003WO-NZ000199.

09-SEP-2002; 2002US-0409557P.

(GENE-) GENESIS RES & DEV CORP LTD.

(WRIG-) WRIGHTSON SEEDS LTD.

Demmer J, Shenk MA, Hall C, Fish SA;

WPI; 2004-248453/23.

N-PSDB; ADM41470.

New antifreeze proteins and encoding polynucleotides, useful for

modulating cold tolerance in organisms, as food additives, or for

treating tumors or disorders associated with the presence of unwanted

biocrystals (e.g. gout).

Claim 7; SEQ ID NO 26; 71pp; English.

The present sequence is that of an antifreeze protein of perennial

ryegrass. The invention provides forage grass (perennial ryegrass and

tall fescue) antifreeze proteins and the polynucleotides encoding them

ADM41458-ADM41483. The polynucleotides were isolated from tissues taken

at different times of year (winter and spring) and from different parts

of the plants. The polynucleotides can be used to modulate the cold

tolerance of an organism, especially plants, mammals, insects, fungi,

archaea and bacteria. The method involves incorporating an antifreeze

polynucleotide, under the control of a gene promoter sequence, into the

genome of the organism, or introducing double-stranded RNA corresponding

to the polynucleotide into the cells of the organism, thereby inhibiting

expression of an antifreeze polypeptide. The antifreeze protein can be

used for the cryopreservation of a cell or tissue, as a food additive of

a frozen food product, in a method for decreasing the time required to

dehydrate a composition, to treat a disorder characterised by biocrystals

associated with disorders such as gout and kidney stones, to preserve the

viability of a molecular biology reagent, to destroy unwanted tissue in a

patient e.g. tumour tissue, and to protect a plant from damage due to

frost or freezing.

Sequence 281 AA;

Query Match 65.3%; Score 904.5; DB 8; Length 281;

Best Local Similarity 66.5%; Pred. No. 1.8e-71;

Matches 187; Conservative 20; Mismatches 51; Indels 23; Gaps 5;

QY 5 MAKCCMLLVFLGFIQVAGATSWCHDDHLAGRLAENLSCGKAVRLRAAGSCCSCW 64

DB 1 MAKCCMLLVFLVLLPAAAT--SCHPDDLRLRGFVGNLNG--GGVLLHGAWSGLCCAW 57

QY 65 EGVGCETASGRVVALRLP-----KRLGGIIPSSIGELDLHRLYDLDSNS 109

DB 58 EGVGCETASGRVVALRLPISLEDCGKLSINLANERLVGTIPSWIGELDHCHVILSDNS 117

QY 110 LVGEVPSLQIRKSLITDSQSLMGSIINMLHV--SSRRTLDEPNTTSGTNNVSG 164

DB 118 LVGKVPNSLQIRKSLITDSQSLMGSIINMLHV--SSRRTLDEPNTTSGTNNVSG 177

Qy 165 SGNVNVGNDNTVSGNNHVSNNVTGSDNTVSGNHVSGTKHIVTDNNVSG 224
Db 178 SGNDAVSGNDNTVICNNNTVSGSNNITASGSDNIVTSGNHVCGTKHIIITDNNVSG 237
Qy 225 NDNVSGSFHTVSGHNTVSGSNNITVSGNHVSGSKVVT 265
Db 238 NDNVSGSFHTVSGHNTVSGSNNITVSGNHVSGSKVVT 278

RESULT 9
ADM41475
ID ADM41475 standard; protein; 281 AA.
XX AC ADM41475;
XX 03-JUN-2004 (first entry)
XX Perennial ryegrass antifreeze protein AFP3.
XX Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;
XX antitoxin; litholytic; nephrotropic; cytostatic.
XX Lolium perenne.
XX Key Location/Qualifiers
XX Peptide 1..19 /label= Signal_peptide
XX Region 10..22 /note= "Conserved lipoprotein membrane attachment site"
XX Region 53..64 /note= "Conserved Cys-pairs identified N-terminal or
XX leucine-rich repeats of receptor-like kinases"
XX Region 69..125 /note= "Conserved leucine-rich repeats"
XX Region 165..279 /note= "7-amino acid sequence repeat region identified in
XX antifreeze proteins"

XX WO2004022700-A2.
XX 18-MAR-2004.
XX 09-SEP-2003; 2003WO-NZ000199.
XX 09-SEP-2002; 2002US-0409557P.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX (WRIG-) WRIGHTSON SEEDS LTD.
XX Demmer J, Shenk MA, Hall C, Fish SA;
XX WPI; 2004-248453/23.
XX N-PSDB; ADM41462.
XX New antifreeze proteins and encoding polynucleotides, useful for
XX modulating cold tolerance in organisms, as food additives, or for
XX treating tumors or disorders associated with the presence of unwanted
XX biocrystals (e.g. gout).
XX Claim 7; SEQ ID NO 18; 71pp; English.
XX The present sequence is that of AFP3, an antifreeze protein of perennial
XX ryegrass. The encoding cDNA was isolated from a root cDNA expression
XX library. The invention provides forage grass (perennial ryegrass and tall
XX fescue) antifreeze proteins and the polynucleotides encoding them
XX (ADM41458-ADM41483). The polynucleotides were isolated from tissues taken
XX at different times of year (winter and spring) and from different parts
XX of the plants. The polynucleotides can be used to modulate the cold
XX tolerance of an organism, especially plants, mammals, insects, fungi,
XX archaea and bacteria. The method involves incorporating an antifreeze
XX polynucleotide, under the control of a gene promoter sequence, into the
XX genome of the organism, or introducing double-stranded RNA corresponding
XX to the polynucleotide into the cells of the organism, thereby inhibiting

CC expression of an antifreeze polypeptide. The antifreeze protein can be
CC used for the cryopreservation of a cell or tissue, as a food additive of
CC a frozen food product, in a method for decreasing the time required to
CC dehydrate a composition, to treat a disorder characterised by biocrystals
CC associated with disorders such as gout and kidney stones, to preserve the
CC viability of a molecular biology reagent, to destroy unwanted tissue in a
CC patient e.g. tumour tissue, and to protect a plant from damage due to
CC frost or freezing.
XX Sequence 281 AA;
XX Query Match 65.1%; Score 901.5; DB 8; Length 281;
XX Best Local Similarity 66.2%; Pred. No. 3.4e-71;
XX Matches 186; Conservative 21; Mismatches 51; Indels 23; Gaps 5;
Qy 5 MAKCCMLVFLGFIQVAGATSWCHDDHLALRGLAENLKGAVRLRAAASGASCCSW 64
Db 1 MAKCCMLLFLVFLLLMSAT--SCHLDDLRALRGVGNLGGAL-LRGTWSSGCCDW 57
Qy 65 EGVGCTASGRVVALRLP-----KRLGGLIIPSSIGELDHLRYLDLSGNS 109
Db 58 EGVGCDGTSGRVTALRLPISLEDCGKLSLNLANERLVGTIPSWIGELDHHCVLSDNS 117
Qy 110 LVGEVP----KSLQIRLKSLLTDSQSLGMSINMLLV--SSRRLDEEPTISGTNSVG 164
Db 118 LVGKAPNSLHNSLQIRLKLATAGRSGLMAFANMPLHVKNRRLDQNTIHGTNTVR 177
Qy 165 SGNVNVGNDNTVSGNNHVSNNVTGSDNTVSGNHVSGTKHIVTDNNVSG 224
Db 178 SGNDAVSGNDNTVICNNNTVSGSNNITASGSDNIVTSGNHVCGTKHIIITDNNVSG 237
Qy 225 NDNVSGSFHTVSGHNTVSGSNNITVSGNHVSGSKVVT 265
Db 238 NDNVSGSFHTVSGHNTVSGSNNITVSGNHVSGSKVVT 278

RESULT 10
ADM41479
ID ADM41479 standard; protein; 285 AA.
XX AC ADM41479;
XX 03-JUN-2004 (first entry)
XX Tall fescue antifreeze protein.
XX Antifreeze; fescue; cold tolerance; transgenic; plant; antitoxin;
XX litholytic; nephrotropic; cytostatic.
XX Schedonorus arundinaceus.
XX Key Location/Qualifiers
XX Peptide 1..17 /label= Signal_peptide
XX Region 12..22 /note= "Conserved lipoprotein membrane attachment site"
XX Region 52..63 /note= "Conserved Cys-pairs identified N-terminal or
XX leucine-rich repeats of receptor-like kinases"
XX Region 68..134 /note= "Conserved leucine-rich repeats"
XX Domain 134..158 /note= Transmembrane domain
XX Region 170..284 /note= "7-amino acid sequence repeat region identified in
XX antifreeze proteins"

XX WO2004022700-A2.
XX 18-MAR-2004.
XX 09-SEP-2003; 2003WO-NZ000199.
XX

XX	Herbicidally active polypeptide SEQ ID NO 3015.
DE	Herbicidal; plant; agriculture; herbicide.
XX	Arabidopsis thaliana.
XX	WO200210210-A2.
XX	07-FEB-2002.
XX	28-AUG-2001; 2001WO-EP009892.
XX	28-AUG-2001; 2001WO-EP009892.
XX	(FARB) BAYER AG.
PA	Tietjen K, Weidler M;
PI	WPI; 2002-269010/31.
XX	Identifying plant target proteins for herbicidally active compounds,
PT	comprising aligning and comparing nucleic acid or amino acid sequences
PT	from plant with nucleic acid or amino acid sequences from non-plant
PT	organisms.
XX	Claim 5; SEQ ID NO 3015; 26lpp + Sequence Listing; English.
XX	The invention relates to identifying target proteins (ABB90790-ABB94016)
CC	for herbicidally active compounds, comprising aligning and comparing
CC	nucleic acid or amino acid sequences from plant with nucleic acid or
CC	amino acid sequences from non-plant organisms using suitable search
CC	parameters, where plane of most similar non-plant sequences are selected.
CC	of 3 than the E-value greater by a factor
CC	The polypeptides or nucleic acids encoding them are useful for
CC	identifying modulators. The identified modulators are useful as
CC	herbicides
XX	Sequence 1036 AA;
SQ	Query Match 18.7%; Score 258.5; DB 5; Length 1036;
	Best Local Similarity 30.7%; Pred. No. 1.6e-13;
	Matches 89; Conservative 50; Mismatches 98; Indels 53; Gaps 14;
Qy	10 MLLVFLGLIQVAGATSWCHHDLHALRGLAENLSGKGAVRLRAAW-SGASCCSWEGVG 68
Dd	5 LLLVFF-----VGSSVSQPCHPNDLSALRELAKKNKSVTE---SWLNGSRCCEDWDGVF 56
Qy	69 CE--TAGRVVALPKRKGGIIPSSIGELDHLRYLDLSGNLSVGEVPKSL----QIRL 122
Dd	57 CEGSDVSGRVTKVLPLPEKLGEGVTSKSIGLETLRVLDSRNQLKGFAPBISKLEQLQV 116
Qy	123 KSLTTDSQSILGWGSINMLLVHSRRRTIDEEPNTISGTNNNSVG-----SGSNNVVSG 173
Dd	117 LDL----SHNLLSGSVLGVSGKLIIQSNISSNLGSKLSDVGPFGVLMLNVSNLNLFEG 173
Qy	174 NDNTW----SGNNNHVSGNNVTGSDNTVGSNNHVSVGTGKHIVTDNNNVVSG----- 224
Dd	174 EIHFELCSSSGGIQVIDLSMNRVGNLD---GLYNCSESKIQLHIDSNRLTGQLPDLYL 229
Qy	225 -----NDNNVSGSFHTYSGEHNTVGSGNNVTGSGNNHIVSGSNK-----VVTD 266
Dd	230 SIRELEQLSLSGNTY--LSGE---LSKNLSNLGSLKSLNISNRPSDVDPD 274

Search completed: May 9, 2005, 20:20:40
Job time : 78 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2005, 22:28:53 ; Search time 3912 Seconds
(without alignments)
9535.528 Million cell updates/sec

Title: US-10-657-852A-3
Perfect score: 980
Sequence: 1 gcttcattcccaatcaagt.....cccttacataaaaaaaa 980

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gsa1:*
- 9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	372.8	38.0	767	4	BJ451048 BJ451048
C 2	372.4	38.0	746	4	BJ458554 BJ458554
C 3	370.2	37.8	686	4	BJ461731 BJ461731
C 4	370.2	37.8	699	4	BJ461803 BJ461803
C 5	366.6	37.4	687	4	BJ459099 BJ459099
C 6	365.6	37.3	693	4	BJ457564 BJ457564
C 7	365.6	37.3	696	4	BJ461908 BJ461908
C 8	362.4	37.0	588	2	BE490074 WHE0365 G
9	362.2	37.0	632	4	BJ453251 BJ453251
10	359.4	36.7	671	4	BJ454271 BJ454271
C 11	357.6	36.5	684	4	BJ462238 BJ462238
C 12	357.2	36.4	609	4	BJ450137 BJ450137
C 13	357.2	36.4	689	4	BJ458121 BJ458121
C 14	352	35.9	692	2	BF474043 WHE0840 D
C 15	348.2	35.5	703	2	BE705098 Sc02_07E0
16	347	35.4	625	4	BJ448772 BJ448772
17	347	35.4	726	4	BJ451602 BJ451602
18	347	35.4	726	4	BJ454431 BJ454431
C 19	346.4	35.3	830	2	BE705403 Sc02_12C0
C 20	344.4	35.1	663	4	BJ461352 BJ461352
C 21	340.4	34.7	830	2	BE705439 Sc02_12G1
C 22	335.6	34.2	1115	7	CK214468 FGAS02639
23	332.6	33.9	841	4	BJ224369 BJ224369
24	331.6	33.8	851	4	BJ448689 BJ448689

C 25	328.8	33.6	675	4	BJ460799 BJ460799
C 26	325.4	33.2	724	4	BJ456413 BJ456413
C 27	323	33.0	620	4	BJ447068 BJ447068
28	322.2	32.9	589	1	AV909087 AV909087
29	318.6	32.5	862	4	BJ454200 BJ454200
C 30	316.2	32.3	818	7	CK197682 FGAS00616
C 31	310.8	31.7	775	2	BE705684 SC01_11G0
C 32	301.6	30.8	709	4	BJ453816 BJ453816
C 33	296.8	30.3	648	4	BJ300903 BJ300903
C 34	296	30.2	574	1	AV910970 AV910970
C 35	294.6	30.1	914	7	CK156167 FGAS03708
C 36	294	30.0	612	1	AV911379 AV911379
C 37	293.6	30.0	581	4	BM376553 ERem05 SQ
C 38	292.8	29.9	480	4	BJ453528 BJ453528
39	285	29.1	588	1	AJ460325 AJ460325
C 40	277.8	28.3	622	1	AU251218 AU251218
C 41	275.8	28.1	585	4	BI479842 WHE3452 G
C 42	275	28.1	841	7	CK196896 FGAS00536
C 43	263.2	26.9	532	2	BF200590 WHE0825-0
C 44	255.6	26.1	420	1	AJ460320 AJ460320
45	255.6	26.1	420	1	AJ460322 AJ460322

ALIGNMENTS

RESULT 1
BJ451048 767 bp mRNA linear EST 23-MAY-2002
LOCUS BJ451048 K. Sato unpublished cDNA library, cv. Akashinriki
DEFINITION vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
baak32h16 5', mRNA sequence.
ACCESSION BJ451048.1 GI:21129647
VERSION BJ451048
KEYWORDS EST
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 767)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
JOURNAL
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6856
Email: tshini@genes.nig.ac.jp.

FEATURES

source
1..767
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Akashinriki"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="baak32h16"
/tissue_type="leaves"
/dev_stage="vegetative stage"
/clone_lib="K. Sato unpublished cDNA library, cv.
Akashinriki vegetative stage leaves"

ORIGIN

Query Match 38.0%; Score 372.8; DB 4; Length 767;
Best Local Similarity 73.5%; Pred. No. 4.2e-100;
Matches 524; Conservative 0; Mismatches 168; Indels 21; Gaps 3;
Qy 233 GTGGGATCGAACAGCGCGCGTGGCGCTTGGCGTCCCGCGCGCTT 292
Db 27 GNAGCATCTTGGCAGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTT 86

```

QY 293 GGAGGGATCCATCCATCGTGGTGGAGCTTGATCACCCTTCGCTATTTGGATCTCTCG 352
Db 87 GTTGGACCATCCCGTCATGGATTGGCGAGCTTGACCACTTTACTACTTGGAATCTTTCG 146
QY 353 GGTAAATCATTTGGTTGGGGAGGTACCAAAAAGTTTGCAGATPACGGCTCAAGAGCCTCAC 412
Db 147 GATAATTCATTTGGTTGGCGAGGTACCCCAAGAGTTT---GATACGGCTCAAGGGCTTCGCC 203
QY 413 ACTGACAGCCAGTCATCTCGGTATGGTTCATTAACATGCTATTGATGT---GAGCAGT 469
Db 204 ATCGCTGCTGCTTCATCAGGTATGATTTTACTAATCATGCCATTTGATGTGGAGCCCTAAC 263
QY 470 AGAAGACGCTCGATGAGAACCAATACATATACAGGACCAACAATAGTTGGATCA 529
Db 264 AGAAGATGCTCGAGAACCAACAATACATATCTGGAGCAACAACATGTCAGATCT 323
QY 530 GGGAGCAACAATTTGTTTCCGGGAATGACAACACGGTCTGATCTGGGAATPAAACCAAT 589
Db 324 GGGAGCAACAATTTGTTTCCGGGAACGACAACACTGTTCATATCCGGGAACAACAAT 383
QY 590 GTGCTGGGAGCAACAACACTGTTGTAATCTGGAAGTGACAATACTGTAGTTGGTAGCAAC 649
Db 384 GTGGCTGGGAGCAACAACACTATGCTAACCGGGAACGACAATACCGTAACCTGGTAGCAAC 443
QY 650 CATGCTGATCAGGACCAACATATGTTTACTGATAACAATAATTTGTTATCCGGGAAC 709
Db 444 CATGCTGATCTGGGACCAACAATATGTAATCTGACAACAACAATGCGGTATCCGGGAAT 503
QY 710 GACAATATGTTCTGGAAGCTTCATATCTGTATCAGGGGAGCAACAATACCGTATCCGGG 769
Db 504 GACAATATGATCTGGGAGTTTCCATACCGTATCCGGGAAGCCACAATCTGTATCTGGG 563
QY 770 AGCAACAATACTGTATCCGGGAGCAACAATATGTAATCTGGAAGCAACAATGCTGAACA 829
Db 564 ACCAACAACACTGTATCTGGGAACAACAATGCTGTAATCTGGGAGCAACAATGCTGAGGA 623
QY 830 GATGTTAATAT-----TCTGTAGTGCAGGATGCTTCCATCTTCCAA 874
Db 624 GATGATGATTTGTAAGTGGAGTGCTCATCTTCGTGAGGAGCTCACCCTTGTTCGGA 683
QY 875 GTTCAGTGTAGTTACAATCAATAGATGGAGCAATACGTTATGTAACTTCA 927
Db 684 GTTCGTTAGTCTACATCACTTGTGGGCGCAATCGTGTATGTAACTTCA 736

```

RESULT 2

BJ458554/c
LOCUS BJ458554 K. Sato unpublished cDNA library, cv. Akashinriki
DEFINITION vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baak32h16 3', mRNA sequence.

ACCESSION

VERSION BJ458554
KEYWORDS GI:21137090

SOURCE

ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.
1 (bases 1 to 746)
Sato, K., Saieho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@gene.nig.ac.jp.
Location/Qualifiers
1..746
/organism="Hordeum vulgare subsp. vulgare"

REFERENCE

AUTHORS Sato, K., Saieho, D. and Takeda, K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@gene.nig.ac.jp.
Location/Qualifiers
1..746
/organism="Hordeum vulgare subsp. vulgare"

FEATURES

source

```

/mol_type="mRNA"
/cultivar="Akashinriki"
/sub_species="vulgare"
/db_xref="taxon:1112509"
/clone="baak32h16"
/tissue_type="leaves"
/dev_stage="vegetative stage"
/clone_lib="K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves"

```

ORIGIN

```

Query Match 38.0%; Score 372.4; DB 4; Length 746;
Best Local Similarity 73.7%; Pred. No. 5.5e-100;
Matches 523; Conservative 0; Mismatches 166; Indels 21; Gaps 3;
QY 236 GGATGCAAAACAGCAAGCGCGCGTCTGGTGGTGGCTCCCAAGCGGGCTTGGGA 295
Db 717 GCATCTCTGGCAGCCCTCGCATGGTTGGAGAGCTCAACCTTGCACAACAAGAGCTT 658
QY 296 GGGATCATCCCATCTCGATTGGTGGCTTGCATCACCCTTCGCTATTTGGATCTCTCGGT 355
Db 657 GGCACCATCCCGTCATGGATTGGGAGCTTGAACCACTTTACTACTTGGATCTTCGGAT 598
QY 356 AATTCAATGGTTGGGGAGGTACCAAAAAGTTTGCAGATACGGCTCAAGAGCCTCACCACT 415
Db 597 AATTCAATGGTTGGCGAGGTACCCCAAGAGTTT---GATACGGCTCAAGGGCTTCGCCATC 541
QY 416 GACAGCCAGTCACTCGGTATGGGTTCCATTAACATGCTATTTGCATGT---GAGCAGTAGA 472
Db 540 GCTGCTGTTTCATCAGGTATGATTTTACTAATGCCATTTGTATGGAGCCCTAAACAGA 481
QY 473 AGAACGCTCGATGAAGAACCAATAACAATACAGGGACCAACAATAGTGTGGATCAGGG 532
Db 480 AGAATGCTCGAGCAACAACAATACAATATCTGGGAGCAACAACATCTGCATCTGGG 421
QY 533 AGCAACAATGTTGTTCCGGGAATGACAACAACGGTCTGATCTGGGAATAACAACATGTG 592
Db 420 AGCACCAATGTTGTTTCTGGGAACGACAACAACATCTCCGGGAACAACAATGTG 361
QY 593 TCTGGGAGCAACAACACTGTTGTAATCTGGAAGTGACAATACTGTAGTTGGTAGCAACCAT 652
Db 360 GCTGGGAGCAACAACACTATCTGTAACCGGGAACGACAATACCGTAACTGTGTAGCAACCAT 301
QY 653 GTCGTATCAGGACAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGAC 712
Db 300 GTCGTATCTGGGACAACAATATCTGTAATCTGACAACAACAATGCCGTATCCGGGAATGAC 241
QY 713 AATAATGTTCTGGAAGCTTTCCATATCTGTATCAGGGGAGCAACAATACCGTATCCGGGAGC 772
Db 240 AATAATGTTATCTGGAGTTTCCATATACCGTATCCGGGAAGCCACAATACTGTATCTGGGAGC 181
QY 773 AACAACTACTGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAGTCGTAAACAGAT 832
Db 180 AACAACTACTGTATCTGGGACAACAACCATGTGTATCTGGGAGCAACAAGTCGTAGGAGAT 121
QY 833 GGTAAATAT-----TCTGTAGTGCAGGATTTGCTTCCATCTTCCCAAGTT 877
Db 120 GCATGATTTGTAAGTGGAGTGCTCCATCTTCGTGACGGAGCTCACCCTTGTGTCCGAGTT 61
QY 878 CAGTGTAGTTTACAATCAATAGATGGAGACAATCACGTTATGTAACTTCA 927
Db 60 CGGTGTAGTCTACAATCACTTGTGGGGCCCAATCGTGTATGTAACTCTCA 11

```

RESULT 3

BJ461731/c

LOCUS BJ461731

DEFINITION vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baak46i20 3', mRNA sequence.

ACCESSION BJ461731

VERSION BJ461731.1

KEYWORDS GI:21140241

686 bp mRNA linear EST 23-MAY-2002
K. Sato unpublished cDNA library, cv. Akashinriki
vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone

QY	857	TTGCTTCCATCTTCCAGTTTCAGTTAGCTTACAATCAATAGATGAGACATCAGCTT	916
Db	87	GCTCACTTGTGTGTCGAGTTTCGCTGTAGCTTCAATCACTTGGTGGGCAATCGTGT	28
QY	917	ATGTAACCTTCA	927
Db	27	ATGTAACCTTCA	17
RESULT 4			
LOCUS	BJ461803/c		
DEFINITION	BJ461803 K. Sato unpublished cDNA library, cv. Akashinriki		
ACCESSION	BAAK46N01.3		
VERSION	BJ461803		
KEYWORDS	EST		
SOURCE	Hordeum vulgare subsp. vulgare		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.		
REFERENCE	1 (bases 1 to 699)		
AUTHORS	Sato, K., Saisho, D. and Takeda, K.		
TITLE	Barley EST sequencing project in NIG and Okayama Univ		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Tadasu Shin-i National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.		
FEATURES			
source	1..699		
ORIGIN			
Query Match	37.8%;	Score 370.2; DB 4; Length 699;	
Best Local Similarity	75.6%;	Pred. NO. 2.5e-99;	
Matches	507;	Conservative 0; Mismatches 143; Indels 21; Gaps 3;	
QY	275	CTCCCCAGCGCGCTTGGAGGATCATCCATCGTGTGAGTTGAGCTTGATCAGCTT	334
Db	686	CTTGCCCAACACAGACTGGTGGCCACCATCCGTCATGATGGCGAGCTTGACACCTT	627
QY	335	CGCTATTTGGATCTCTCGGTAATTCATTGTGGTGGGAGGTACCAAAAAGTTTCAGATA	394
Db	626	TACTACTTGGATCTTTGGGTAATTCATTGTGGTGGGAGGTACCCAGAGTTT---	570
QY	395	CGGCTCAAGAGCCTTCAACCTGACAGCCAGTCACCTCGGTATGGGTTCATTAACATGCTA	454
Db	569	CGGCTCAAGGGCTTCGCCATCGTGTTCATCAGGTATGATTTTCTACTAACATGCCA	510
QY	455	TTGCATGT---	511
Db	509	TTGTATGTGGAGCCCTTAACAGAGAGATGCTCGACGAAACCAATATCTCTGGGAGC	450
QY	512	ACCAATAGTGTGGATCAGGAGCAACAAATGTTTTCGGGAAATGACAAACCGTCTGA	571
Db	449	ACCAACACTGTGAGATCTGGGAGCAACCAATGTTTCTGGGAGCAACCACTGTCTATA	390


```
FEATURES
  source
    Location/Qualifiers
      1..693
        /organism="Hordeum vulgare subsp. vulgare"
        /mol_type="mRNA"
        /cultivar="Akashinriki"
        /sub_species="vulgare"
        /db_xref="taxon:112509"
        /clone="baak21d01"
        /issue_type="leaves"
        /dev_stage="vegetative stage"
        /clone_lib="K. Sato unpublished cdna library, cv.
        Akashinriki vegetative stage leaves"

ORIGIN
  Query Match      37.3%; Score 365.6; DB 4; Length 693;
  Best Local Similarity 75.3%; Pred. No. 5.9e-98;
  Matches 503; Conservative 0; Mismatches 144; Indels 21; Gaps 3;

QY 275 CTCCTCAAGCGGCGCTTGAGGAGATCATCCCATCGTATGGTGGAGCTTGATCAACCTT 334
DB |||
DB 685 CTTGCCAACACAGACTGGTTGGCACCCTCCCGTCATGGATTGGCGAGCTTGACCACCTT 626
QY 335 CGCTATTTCGATCTCTCGGTAATTCATTTGGTGGGAGGTACCAAAAGTTTGCAGATA 394
DB |||
DB 625 TACTACTTGGATCTTTTCGGATAATTCATTTGGTGGGAGGTACCCCAAGAGTTT---GATA 569
QY 395 CGGCTCAAGAGCGCTCAACCACTGACGCCAGTCACTCGGTATGGTTTCCATTAAACATGCTA 454
DB |||
DB 568 CGGCTCAAGGCGTTCCGCCATCGCTGCTGTTTCATCAGGTATGATTTTACTAACATGCCA 509
QY 455 TTGCATGT---GAGCAGTAGAAGACGCTGCGATGAAGAACCAAAATCAATATCAGGGAGC 511
DB |||
DB 508 TTGTATGTGGAGCCTAACAGAAATGCTCGACGAACAACCAATACAATATCTGGGAGC 449
QY 512 AACATAGTGTGGATCAGGAGCAACAATGTTTTCGGGATCAGCAACACGTCGTA 571
DB |||
DB 448 AACCAACTGTCTGATCTGGGAGCAACAATGTTTTCGGGAGCAACAACACTGTCTGTCATA 389
QY 572 TCTGGGAATAACAAACCACTGTCTGGGAGCAACAACACTGTTGTAACCTGGAGTGAACAT 631
DB |||
DB 388 TCCGGGACACAAACAATGTGGCTGGGAGCAACAACACTATCGTAACCGGGACGACAT 329
QY 632 ACTGTAGTTGGTAGCAACCATGCTGATCAGGGAACAAGCATATGTTTACTGATAACAAT 691
DB |||
DB 328 ACCGTAACCTGGTAGCAACCATGCTGATCTGGGACAAACATATCTGTAACCTGACAAAC 269
QY 692 AATGTTGTATCCGGGAGCAACAATATGCTGGAAGCTTCCATCTGATCTGATCAGGGAG 751
DB |||
DB 268 AATGCCGTATCCGGGAATGCAATATGATCTGGAAGTTTCCATACCGTATCCGGAGC 209
QY 752 CACAATACCGTATCCGGGAGCAACAATCTGATCTGGGAGCAACAACATATCGTATCTGGG 811
DB |||
DB 208 CACAACTCTGTATCTGGGACCAACAACACTGTAATCTGGGAACAACCAATGCTGATCTGG 149
QY 812 AGCAACAAGTCTGTAACAGATGTTTAATAT-----TCTGTAGTGTGACGA 856
DB |||
DB 148 AGCAACAAGTCTGTAAGATGATGATTTGTAAGTGGAGTGCCATCTTCGTGACGGA 89
QY 857 TTGCTTCCATCTTCCCAAGTTAGTGTAGCTTCAATCAATAGATGAGACAAATACGTT 916
DB |||
DB 88 GCTCACTGTTTGTTCGGAGTTCCGTGTAGTCTCAATCACTTGGTGGGCGCAATCGTGT 29
QY 917 ATGTAACCT 924
DB |||
DB 28 ATGAACCT 21

RESULT 7
BJ461908/c 696 bp mRNA linear EST 23-MAY-2002
LOCUS BJ461908 K. Sato unpublished cdna library, cv. Akashinriki
DEFINITION vegetative stage leaves Hordeum vulgare subsp. vulgare cdna clone
baak21d01 3', mRNA sequence.
```

```
ACCESSION BJ461908
VERSION BJ461908.1 GI:21140417
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 696)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadabu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
  1..696
    /organism="Hordeum vulgare subsp. vulgare"
    /mol_type="mRNA"
    /cultivar="Akashinriki"
    /sub_species="vulgare"
    /db_xref="taxon:112509"
    /clone="baak21d01"
    /issue_type="leaves"
    /dev_stage="vegetative stage"
    /clone_lib="K. Sato unpublished cdna library, cv.
    Akashinriki vegetative stage leaves"

ORIGIN
  Query Match      37.3%; Score 365.6; DB 4; Length 696;
  Best Local Similarity 75.3%; Pred. No. 5.9e-98;
  Matches 503; Conservative 0; Mismatches 144; Indels 21; Gaps 3;

QY 275 CTCCTCAAGCGGCGCTTGAGGAGATCATCCCATCGTATGGTGGAGCTTGATCAACCTT 334
DB |||
DB 683 CTTGCCAACACAGACTGGTTGGCACCCTCCCGTCATGGATTGGCGAGCTTGACCACCTT 624
QY 335 CGCTATTTCGATCTCTCGGTAATTCATTTGGTGGGAGGTACCAAAAGTTTGCAGATA 394
DB |||
DB 623 TACTACTTGGATCTTTTCGGATAATTCATTTGGTGGGAGGTACCCCAAGAGTTT---GATA 567
QY 395 CGGCTCAAGAGCGCTCAACCACTGACGCCAGTCACTCGGTATGGTTTCCATTAAACATGCTA 454
DB |||
DB 566 CGGCTCAAGGCGTTCCGCCATCGCTGCTGTTTCATCAGGTATGATTTTACTAACATGCCA 507
QY 455 TTGCATGT---GAGCAGTAGAAGACGCTCGATGAAGAACCAAAATACAATATCAGGGAGC 511
DB |||
DB 506 TTGTATGTGGAGCCTAACAGAAATGCTCGACGAACAACCAATACAATATCTGGGAGC 447
QY 512 AACATAGTGTGGTAGTACGGGAGCAACAATGTTTTCGGGGAATGACAAACAGCTGCTA 571
DB |||
DB 446 AACCAACTGTCTGATCTGGGAGCAACAATGTTTTCGGGAGCAACAACACTGTCTGTCATA 387
QY 572 TCTGGGAATAACAAACCACTGTCTGGGAGCAACAACACTGTTGTAACCTGGAGTGAACAT 631
DB |||
DB 386 TCCGGGAACAACAACAATGTGGCTGGGAGCAACAACACTATCGTAACCGGGAGCAACAAT 327
QY 632 ACTGTAGTTGGTAGCAACCATGCTGCTGATCAGGGAACAAGCATATGTTTACTGATAACAAT 691
DB |||
DB 326 ACCGTAACCTGGTAGCAACCATGCTGCTGATCTGGGACAAACATATCGTAACCTGACAAAC 267
QY 692 AATGTTGTATCCGGGAGCAACAATATGCTGGAAGCTTCCATCTGATCTGATCAGGGAG 751
DB |||
DB 266 AATGCCGTATCCGGGAATGCAATATGATCTGGAAGTTTCCATACCGTATCCGGAGC 207
QY 752 CACAATACCGTATCCGGGAGCAACAATCTGATCTGGGAGCAACAACATATCGTATCTGGG 811
DB |||
DB 206 CACAATACTGTATCTGGGAGCAACAACACTGTATCTGGGAGCAACAACATGCTGATCTGGG 147
```

QY 812 AGCAACAAAGTCGTACACAGATGGTTAATAT-----TCTGTAGTGCAGGA 856
 |||||
 Db 146 AGCAACAAAGTCGTAGAGATGATGATTTGTAAGTGGAGTGTCCATCTTCGTGACGGA 87
 |||||
 QY 857 TTGCTTCCATCTTCCCAAGTTCAGTGTAGCTTACCAATCAATAGATGGAGACAATCAAGTT 916
 |||||
 Db 86 GCTCACCTTGTGTCGAGTTCGGTGTAGCTCACATCACTTGGTGGGCCAATCGTGT 27
 |||||
 QY 917 ATGTAAC 924
 |||||
 Db 26 ATGAACCT 19

BE490074 588 bp mRNA linear EST 31-JUL-2000
 WHE0365 G07 N13ZS Wheat cold-stressed seedling cDNA library
 LOCUS Triticum aestivum cDNA clone WHE0365_G07_N13, mRNA sequence.
 DEFINITION BE490074
 ACCESSION BE490074.1 GI:9609607
 VERSION EST
 KEYWORDS Triticum aestivum (bread wheat)
 SOURCE Triticum aestivum
 ORGANISM Triticum aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 588)

AUTHORS Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D.,
 Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
 Seaton, C.L. and Tong, J.C.
 TITLE The structure and function of the expressed portion of the wheat
 genomes - Cold-stressed seedling cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818

Email: oanderson@pw.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: Stratagene SK primer.

FEATURES
 source

Location/Qualifiers
 1..588

/organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE0365_G07_N13"
 /tissue_type="Seedling"
 /dev_stage="Five-day old seedling"
 /lab_host="E. coli SOLR"
 /clone_lib="Wheat cold-stressed seedling cDNA library"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
 Site 1: EcoRI; Site 2: XhoI; Seeds were
 surface-sterilized, germinated and grown aseptically in
 the dark at room temperature on filter paper with water,
 nystatin and cefotaxime in covered crystallization
 dishes. Five-day old seedlings were transferred to 5 C
 cold room and kept for 48 hr. The tissue, total RNA, and
 poly(A) RNA were prepared, a cDNA library was made, and
 the cDNA clones were in vivo excised to give pBluescript
 phagemids in the TJ Close lab (Choi, Close, Fenton) at
 the University of California, Riverside. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."

ORIGIN

Query Match 37.0%; Score 362.4; DB 2; Length 588;
 Best Local Similarity 79.5%; Pred. No. 5.2e-97;
 Matches 455; Conservative 0; Mismatches 111; Indels 6; Gaps 2;

QY 257 CGCGTGTGCGCTTGGCGCTCCCCAAGCGCGGCTTGGAGGATCATCCCATCTCGATT 316
 |||||
 Db 20 CGGCTAGAGGAGCTCAACCTTGGCCAAACAACAACTGGTCGGTACCATCCCATCTGGATT 79
 |||||
 QY 317 GGTGAGCTTGATACCTTCGCTATTTCGATCTCTCGGGTATTTCATTGGTTGGGAGGTA 376
 |||||
 Db 80 GCGGAGCTTGATACCTTTTGTCTACTTGGATCTGCGGATTAATTATTGGTTGGGAGGTA 139
 |||||
 QY 377 CCAAAAAGTTTGCAGATACGGCTCAAGAGCTCAACCACTGACAGCCAGTCACTCGGTATG 436
 |||||
 Db 140 CCCAAGAGTTT---GATAAGGCTCAAGGCTCTCGTCATCTGGTCTGTTCACTAGGTATG 196
 |||||
 QY 437 GGTTCATTAACATGCTATTTCATGTGA---GCAGTAGAAGAACGCTCGATGAAGAACA 493
 |||||
 Db 197 GTTTTACGAACATGCTCATTTGATGTGAAGCGTAATAGAAGAACACTCGAGAACAAACA 256
 |||||
 QY 494 AATCAATATATCAGGAGCCCAACAATAGTGTGGATCAGGAGCAACAATTTGTTTCGGG 553
 |||||
 Db 257 AATACATATCTGGAGCAACACACTGTAGATCTCGAAGCACCAAGTTGTTCTGGG 316
 |||||
 QY 554 AATCAACACAGCTCGTATCTGGGAATAACAACCATGTCTGGGAGCAACAACACTGTT 613
 |||||
 Db 317 AATGACAACATGTCATATCGGGGAAATAACAACAATGTGGCTGTAGCAACAACACTGTC 376
 |||||
 QY 614 GTAACCTGAGTGAACATCTAGTTGGTAGCAACCATGCTCGTATCAGGAGCAAAAGCAT 673
 |||||
 Db 377 GTAAACCGGGAACAACAATACCGTAACCTGGTAGCAACCATATTGTATCTGGGAGCAACA 436
 |||||
 QY 674 ATTGTTACTGATACAATAATTTGTTATCCGGGAACCAACAATAATGTCTGGAAGCTTC 733
 |||||
 Db 437 ATCGTACTGACATAACATGCGGTATCCGGNATGACAAATATGTATCTGGAGGCTTC 496
 |||||
 QY 734 CATACTGTATCAGGGAGCAACAATACCGTATCCGGGAGCAACAATATCTATCCGGAGC 793
 |||||
 Db 497 CATACCTATCCGGAGCCACAATATCTGTATCTGGGACCAACAACACTGTATCCGGAAGC 556
 |||||
 QY 794 AACCATATCTATCTGGGAGCAACAAGTCGT 825
 |||||
 Db 557 AACCATGTGTATCTGGGAGCAACAAGTCGT 588
 |||||

RESULT 9
 BJ453251

LOCUS
 DEFINITION

BJ453251 632 bp mRNA linear EST 23-MAY-2002
 BJ453251 K. Sato unpublished cDNA library, cv. Akashinriki
 vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
 baak42e04 5', mRNA sequence.

ACCESSION
 VERSION

KEYWORDS
 SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.

REFERENCE

AUTHORS

TITLE

COMMENT

1 (bases 1 to 632)
 Sato, K., Saisho, D. and Takeda, K.
 Barley EST sequencing project in NIG and Okayama Univ
 Unpublished (2002)
 Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.

FEATURES
 source

Location/Qualifiers
 1..632
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Akashinriki"
 /sub_species="vulgare"
 /db_xref="taxon:112509"


```

LOCUS      BJ462238                684 bp    mRNA    linear    EST 23-MAY-2002
DEFINITION      BJ462238 K. Sato unpublished cDNA library, cv. Akashinriki
                vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
                baak24g16 3', mRNA sequence.
ACCESSION      BJ462238
VERSION        BJ462238.1    GI:21140745
KEYWORDS       EST.
SOURCE         Hordeum vulgare subsp. vulgare
ORGANISM       Hordeum vulgare subsp. vulgare
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Poideae; Triticeae; Hordeum.
REFERENCE      1 (bases 1 to 684)
AUTHORS        Sato, K., Saisho, D. and Takeda, K.
TITLE          Barley EST sequencing project in NIG and Okayama Univ
JOURNAL        Unpublished (2002)
COMMENT        Contact: Tadasu Shin-i
                Center For Genetic Resource Information
                National Institute of Genetics
                1111 Yata, Mishima, Shizuoka 411-8540, Japan
                Tel: 81-559-81-6856
                Fax: 81-559-81-6855
                Email: tshini@genes.nig.ac.jp.
FEATURES       Location/Qualifiers
                1..684
                /organism="Hordeum vulgare subsp. vulgare"
                /mol_type="mRNA"
                /cultivar="Akashinriki"
                /sub_species="vulgare"
                /db_xref="taxon:112509"
                /clone="baak24g16"
                /tissue_type="leaves"
                /dev_stage="vegetative stage"
                /clone_lib="K. Sato unpublished cDNA library, cv.
                Akashinriki vegetative stage leaves"
ORIGIN
Query Match      36.5%; Score 357.6; DB 4; Length 684;
Best Local Similarity 78.4%; Pred. No. 1.5e-95;
Matches 455; Conservative 0; Mismatches 11; Indels 6; Gaps 2;

QY 265 GCGCTTGGCGCTCCCAAGCGCGGCTTGGAGGGATCATCCCATGTCGATTTGGTGAGCT 324
DB 679 GGAGCTCAACTTGGCAACACAGACTGGTTGGCACCATCCGTCATGGATTGGCGAGCT 620
QY 325 TGATCACTTCGCTATTGGATCTCTCGGTAATTTCATTTGGTGGGAGGTACCAAAAG 384
DB 619 TGACCACCTTTACTACTTGGATCTTTTCGGATAATTTCATTTGGTTGGCGAGGTACCAAGAG 560
QY 385 TTTGCAGATACGGCTCAAGAGCGCTCACCACCTGCAGCCAGTCACCTCGGTATGGTTCCAT 444
DB 559 TTT---GATACGGCTCAAGGGCTTCGCCATCGTGGTCTGTCATCAGGTATGATTTTAC 503
QY 445 TAACATGCTATTGCATGT---GAGCAGTAGAAGAACGCTCGATGAAGAACCAATAACAAT 501
DB 502 TAACATGCCATTGATGTGGAGCGCTTAACAGAAGAATGCTCGACGAAACAACCAATACAAT 443
QY 502 ATCAGGGACCAACATAGTGTGGATCAGGAGCAACAATGTTTTCGGGGAATGACAA 561
DB 442 ATCTGGGAGCAACAACACTGTGAGATCTGGGAGCACCNAATGTTGTTTCTGGGAACGCAA 383
QY 562 CACGCTCGTATCTGGGAATAACAACATGTCTCTGGGAGCAACAACACTGTTGTAACCTGG 621
DB 382 CACTGTCTATATCCGGGAACAACAACATGTGGCTGGGAGCAACAACACTATCGTAAACGG 323
QY 622 AAGTGACAATATCTGTAGTTGGTAGCAACCATGTGCTATCAGGGACAAAGCATATTTGATC 681
DB 322 GAACGACAATACCGGTAACTGTTAGCAACCATGTGCTATCTGGGACAAACATATCGTAAC 263
QY 682 TGATAACAATAATGTTGTATCCGGGAACGACAATAATGCTGTCTGGAAGCTTCCATCTGT 741
DB 262 TGACAACAACATGCCGATATCCGGGAATGACAATAATGATATCTGGGAGTTTCCATACCGT 203

```

```

QY 742 ATCAGGGAGACACAATACCGTATCCGGAGCAACAATATCTGTATCCGGAGCAACCATAT 801
DB 202 ATCCGGAGGCCACCAATATCTGTATCTGGGACCAACAACACTGTATCTGGGAACAACCATGT 143
QY 802 CGTATCTGGGAGCAACAAGTCGTAACAGATGGTTAATAT 841
DB 142 CGTATCTGGGAGCAACAAGTCGTAAGAGATGCATGATTT 103

RESULT 12
BJ450137
LOCUS      BJ450137                609 bp    mRNA    linear    EST 23-MAY-2002
DEFINITION      BJ450137 K. Sato unpublished cDNA library, cv. Akashinriki
                vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
                baak28d17 5', mRNA sequence.
ACCESSION      BJ450137
VERSION        BJ450137.1    GI:21128743
KEYWORDS       EST.
SOURCE         Hordeum vulgare subsp. vulgare
ORGANISM       Hordeum vulgare subsp. vulgare
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Poideae; Triticeae; Hordeum.
REFERENCE      1 (bases 1 to 609)
AUTHORS        Sato, K., Saisho, D. and Takeda, K.
TITLE          Barley EST sequencing project in NIG and Okayama Univ
JOURNAL        Unpublished (2002)
COMMENT        Contact: Tadasu Shin-i
                Center For Genetic Resource Information
                National Institute of Genetics
                1111 Yata, Mishima, Shizuoka 411-8540, Japan
                Tel: 81-559-81-6856
                Fax: 81-559-81-6855
                Email: tshini@genes.nig.ac.jp.
FEATURES       Location/Qualifiers
                1..609
                /organism="Hordeum vulgare subsp. vulgare"
                /mol_type="mRNA"
                /cultivar="Akashinriki"
                /sub_species="vulgare"
                /db_xref="taxon:112509"
                /clone="baak28d17"
                /tissue_type="leaves"
                /dev_stage="vegetative stage"
                /clone_lib="K. Sato unpublished cDNA library, cv.
                Akashinriki vegetative stage leaves"
ORIGIN
Query Match      36.4%; Score 357.2; DB 4; Length 609;
Best Local Similarity 79.1%; Pred. No. 1.9e-95;
Matches 451; Conservative 0; Mismatches 113; Indels 6; Gaps 2;

QY 275 CTCCCAGCGCGCGCTTGGAGGGATCATCCCATCGTCGATTTGGTGTGATCACCCTT 334
DB 29 CTTCGCCAACACAGACTGGTTGGCACCATCCGTCATGGATTGGCGAGCTTGACCACCTT 88
QY 335 CGCTATTGTGATCTCTCGGTAATTTCATTTGGTGGGAGGTACCAAAAAGTTTGCAGATA 394
DB 89 TACTACTTGGATCTTTTCGGATAATTTCATTTGGTGGGAGGTACCCAGAGTTT---GATA 145
QY 395 CGGCTCAAGAGCTCACCACTGCAGCCAGTCACCTGGTATGGTTCCATTAAACATGCTA 454
DB 146 CGGCTCAAGGGCTTCGCCATCGCTGGTCTGTCATCAGGTATGATTTTACTTAACATGCCA 205
QY 455 TTGCATGT---GAGCAGTAGAAGAACGCTCGATGAAGAACCAATAACAATATCAGGGACC 511
DB 206 TTGTATGTGGAGCCTTAACAGAAGATGCTCGACGAAACAACCAATAACAATATCTGGGAGC 265
QY 512 AACATAGTGTTCGATCAGGGAGCAACATGTTTTCGGGATGACACACACGCTCGTA 571
DB 266 AACAACTCTGAGATCTGGGAGCAACCAATGTTGTTTCTGGGAAACGACAACTGTGTCATA 325
QY 572 TCTGGGAATAACAACCATGTGTCTGGGAGCAACAACACTGTTTGTAACTGGAAGTGACAAT 631

```

Db 326 TCCGGGAACAAACAAATGCGCTGGGAGCAACAACTATCTGAACCGGGAACGCAAT 385
Qy 632 ACTGTAGTTGGTAGCAACCAATGTCGTATCAGGGACAAAGCATATTTACTGATAACAAT 691
Db 386 ACCGTAACCTGAGCAACCAATGTCGTATCTGGGACAAACATATCGTAACCTGACACAC 445
Qy 692 AATGTTGTTATCCGGGAACGACAAATATGTCGTATCTGGGAGCTTCATATCTGATCAGGGAG 751
Db 446 AATGCGGTATCCGGGAATGCAATAATATCTGTTGAGGATTTCCATACCGTATCCGGAAGC 505
Qy 752 CACAATACCGTATCTCCGGGACCAACATATCTGATCTCGGGAGCAACATATCGTATCTGGG 811
Db 506 CACAATACTGATCTGGGACCAACACATGATCTGTTGAGGACCAACATGTCGTATCTGGG 565
Qy 812 AGCAACAAAGTCGTAAACAGATGTTAATAT 841
Db 566 AGCAACAAAGTCGTAGGAGATGATGATTT 595
RESULT 13
BJ458121/c
LOCUS
DEFINITION
vegetative stage leaves Hordeum vulgare subsp. vulgare cdna clone
baak30m05 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE
1 (bases 1 to 689)
Sato, K., Saisho, D., and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Contact: Tadasu Shin-i
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
source
1..689
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Akashinriki"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="baak30m05"
/tissue_type="leaves"
/dev_stage="vegetative stage"
/clone_lib="K. Sato unpublished cdna library, cv.
Akashinriki vegetative stage leaves"
ORIGIN
Query Match 36.4%; Score 357.2; DB 4; Length 689;
Best Local Similarity 79.1%; Pred. No. 2e-95;
Matches 451; Conservative 0; Mismatches 113; Indels 6; Gaps 2;
Qy 275 CTCCCAAGCGCGCTTGGAGGATCATCCCATCGTCGATTCGTGAGCTTGATCACCTT 334
Db 681 CTTGCCACACACAGATGGTGGACCATCCCGTCATGATTCGGAGCTTGACACCTT 622
Qy 335 CGCTATTGGATCTCTCGGGTAATTCATTTGGTGGGAGGTACCAAAAGTTTGCAGATA 394
Db 621 TACTACTGGATCTTTCGGATATTCATTTGGTGGGAGGTACCAAGAGTTT---GATA 565
Qy 395 CGGCTCAAGAGCTCACCATGACAGCCAGTCTCTCGGTATGGTTCATTAACATGCTA 454

Db 564 CGGCTCAAGGCTTCCGCATCGCTGCTGTTCTATCAGGTATGATTTTTTACTAATGCCA 505
Qy 455 TTGCATGT---GAGCAGTAGAAGACGCTCGATGAAGAACCAATATAATATCAGGAGC 511
Db 504 TTGTATGTGGAGCCTAACAGAGATGCTCGACGACCAACCAATATAATATCTGGGAGC 445
Qy 512 AACATAGTTGTTGATCAGGGAGCAACATGTTGTTTCCGGGAATGACAAACACGTCGTA 571
Db 444 AACAAACATGTCAGATCTGGGAGCACCATGTTGTTTCTGGGAACGACAACTGTCTATA 385
Qy 572 TCTGGGAATAAACAAACCATGTCCTGGGAGCAACCAACACTGTTGTAACCTGGAAGTGACAAT 631
Db 384 TCCGGGAACAAACAAATGTTGCTGGGAGCAACACTATCTGAACCGGAGACGACAT 325
Qy 632 ACTGTAGTTGGTAGCAACCAATGTCGTATCAGGGACAAAGCATATTTACTGATAACAAT 691
Db 324 ACCGTAACCTGAGCAACCAATGTCGTATCTGGGACCAACATATCGTAACCTGACAAAC 265
Qy 692 AATGTTGTTATCCGGGAACGACAAATATGTCGTGGAGCTTCATATCTGATCAGGGAG 751
Db 264 AATGCGGTATCCGGGAATGACAAATATGATCTGTTGAGGATTTCCATACCGTATCCGGAAGC 205
Qy 752 CACAATACCGTATCCGGGAGCAACATATCTGATCTCGGGAGCAACCATATCGTATCTGGG 811
Db 204 CACAATACTGATCTCGGACCAACACTGATCTGTTGGAACCAACCATGTCGTATCTGGG 145
Qy 812 AGCAACAAAGTCGTAAACAGATGTTAATAT 841
Db 144 AGCAACAAAGTCGTAGGAGATGATGATTT 115
RESULT 14
BF474043
LOCUS
DEFINITION
WHE0840_D01 H02ZS Wheat vernalized crown cdna library Triticum
aestivum cdna clone WHE0840_D01_H02, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 692)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D.,
Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat
genomes - Vernalized crown cdna library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderan@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stragene SK primer.
FEATURES
Location/Qualifiers
1..692
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0840_D01_H02"
/tissue_type="Crown tissue of seedling"
/dev_stage="Five-week old seedling"
/lab_host="E. coli SOLR"
/clone_lib="Wheat vernalized crown cdna library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;"

Qy 833 GGTTAATAT 841

Db 74 GAATGATT 66

Search completed: May 11, 2005, 01:33:58
Job time : 3917 secs

This Page Blank (uspio)

Result No.	Score	Query		Length	DB	ID	Description
		Match					
C	1	44.8	4.6	3453	4	US-10-101-464A-861	Sequence 861, App
	2	44.8	4.6	7218	1	US-08-232-463-14	Sequence 14, Appl
	3	41	4.2	408	4	US-10-101-464A-212	Sequence 212, App
	4	40.4	4.1	396	4	US-10-101-464A-221	Sequence 221, App
	5	40.4	4.1	3381	3	US-09-336-447A-6	Sequence 6, Appl
C	6	40.4	4.1	3381	4	US-09-952-267B-6	Sequence 6, Appl
	7	38.8	4.0	1028	3	US-09-249-180-1	Sequence 1, Appl
	8	38.8	4.0	1476	3	US-09-434-288-12	Sequence 12, Appl
	9	38.8	4.0	2900	4	US-10-101-464A-840	Sequence 840, App
	10	38.4	3.9	1107	4	US-10-101-464A-268	Sequence 268, App
C	11	38.4	3.9	2735	4	US-10-101-464A-865	Sequence 865, App
	12	38.2	3.9	454	3	US-09-228-986-39	Sequence 39, Appl
	13	38.2	3.9	454	4	US-10-101-464A-39	Sequence 39, Appl
	14	38.2	3.9	498	4	US-10-101-464A-421	Sequence 421, App
	15	38.2	3.9	505	4	US-09-621-976-15639	Sequence 15639, A
C	16	38.2	3.9	1590	4	US-09-248-796A-2600	Sequence 2600, App
	17	38.2	3.9	2691	4	US-10-101-464A-837	Sequence 837, App
	18	38.2	3.9	23210	4	US-09-596-002-17	Sequence 17, Appl
	19	38	3.9	535	3	US-09-056-556-171	Sequence 171, App
	20	38	3.9	535	3	US-09-072-596-166	Sequence 166, App
C	21	38	3.9	535	4	US-09-072-967-171	Sequence 171, App
	22	38	3.9	4403765	3	US-09-103-840A-2	Sequence 2, Appl
	23	38	3.9	4411529	3	US-09-103-840A-1	Sequence 1, Appl
	24	37.4	3.8	4689	3	US-09-105-537-34	Sequence 34, Appl
	25	37.4	3.8	36778	3	US-09-105-537-5	Sequence 5, Appl
C	26	37.4	3.8	38506	4	US-09-320-878-19	Sequence 19, Appl
	27	37.4	3.8	38506	4	US-09-141-908-1	Sequence 1, Appl

ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (79)..(735)
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(1028)
FEATURE:
NAME/KEY: misc feature
LOCATION: (424)..(693)
OTHER INFORMATION: Heat Shock Domain
FEATURE:
NAME/KEY: exon
LOCATION: (1)..(328)
FEATURE:
NAME/KEY: exon
LOCATION: (329)..(1028)
FEATURE:
NAME/KEY: Poly A site
LOCATION: (1028)..(1028)
FEATURE:
NAME/KEY: mRNA
LOCATION: (1)..(1028)
FEATURE:
NAME/KEY: source
LOCATION: (1)..(1028)
OTHER INFORMATION: Zea Mays L., Line B73
FEATURE:
NAME/KEY: transit peptide
LOCATION: (79)..(213)
FEATURE:
NAME/KEY: 3'UTR
LOCATION: (736)..(1028)
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (1)..(78)
PUBLICATION INFORMATION:
AUTHORS: Lund, Adrian A.
AUTHORS: Blum, Paul H.
AUTHORS: Bhattachakki, Dinakar
AUTHORS: Elthon, Thomas E.
TITLE: Heat-Stress Response of Maize Mitochondria
JOURNAL: Plant Physiol.
VOLUME: 116
PAGES: 1097-1110
DATE: 1998-03-00
US-09-249-180-1

Query Match 4.0%; Score 38.8; DB 3; Length 1028;
Best Local Similarity 52.5%; Pred. No. 0.083;
Matches 85; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 175 AGGAGCGCTCCGCTCCGCGCGCATGTCGCGGCGCTCATGTCGAGCTGGGAAGTGT 234
DB 189 AGTAGCGCGCGCTCCGCGCTCAACACCGCGCTCCGCTCCGAGCTACGAGGGGC 248
QY 235 GGGATGCGAAACAGCAAGCGCGCTGTCGGCTGTCGCTCCCAAGCGCGCTTGG 294
DB 249 CGAGTCGAAGACGATAGCTCCGAGTAGACGATGGCGGCGACGCGCGGACTACGC 308
QY 295 AGGATCATCCATCGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCG 336
DB 309 TGTGCCAGCGCTGTTCTCAGATATTTTCCGTGATCCGCTTAG 350

RESULT 8
US-09-434-288-12/c
Sequence 12, Application US/09434288
Patent No. 6303767
GENERAL INFORMATION:
APPLICANT: Betlach C., Melanie
APPLICANT: McDaniel, Robert
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA

TITLE OF INVENTION: CONSTRUCTS THEREFOR
FILE REFERENCE: 30062-20030.00
CURRENT APPLICATION NUMBER: US/09/434,288
CURRENT FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 60/107,093
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 1476
TYPE: DNA
ORGANISM: Streptomyces narbonensis
US-09-434-288-12

Query Match 4.0%; Score 38.8; DB 3; Length 1476;
Best Local Similarity 50.0%; Pred. No. 0.11;
Matches 97; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
QY 85 CATCTTCAGGTGCGCAGGACAGCTGCTGGTGTGCCACGACGACCTCCACGGTT 144
DB 1281 CCTGCCCGCGTGAAGCGGACCGCGGCTCGCTCCACGCGACATCCGCGACGC 1222
QY 145 GAGGGGCTGCTGAGAACCTAAGCGCAAGGAGCGCTCGCTCCGCGCGCATGTC 204
DB 1221 CGACCTCTCGCCGGGAACTGCGGCGCTCGACGCGCTGTCACCTTCGCGCGGAG 1162
QY 205 CGGCGCTCATGTCAGCTGGGAAGGTGGGATGCGAAACAGCAAGCGCGCGCTCGT 264
DB 1161 CCAGCTCGACCGCTCCATCGCGGGGCGCTCGGTTCACCGGACCAACGTCACGAGGCAC 1102
QY 265 GGGTTCGGGCTCC 278
DB 1101 CGAGACCTGCTCC 1088

RESULT 9
US-10-101-464A-840
Sequence 840, Application US/10101464A
Patent No. 8768041
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 840
LENGTH: 2900
TYPE: DNA
ORGANISM: Pinus radiata
US-10-101-464A-840

Query Match 4.0%; Score 38.8; DB 4; Length 2900;
Best Local Similarity 56.2%; Pred. No. 0.16;
Matches 73; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY 274 GCTCCCAAGCGCGCTTGGAGGATCATCCATCGTGTGAGTGGTGTGATCACCT 333
DB 1723 GCTTCTCTACACGCACTTGAAGTCTGTATACAGCTTCAATCAGTGAGCTTCAAATCT 1782
QY 334 TCGCTATTTGGATCTCTCGGGTAATTCATTTGGTGGGAGGTACCAAAAAGTTTGCAGAT 393

```
Db 1783 TCAGGACATGGATTCTCTCCCAACAATGTGAGACTTGAGACTTCAAAGCTTTGATATT 1842
QY 394 ACCGCTCAAG 403
Db 1843 TCCGTTTCATG 1852

RESULT 10
US-10-101-464A-268
; Sequence 268, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10101464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-101-464A-268

Query Match 3.9%; Score 38.4; DB 4; Length 1107;
Best Local Similarity 49.6%; Pred. No. 0.12;
Matches 127; Conservative 0; Mismatches 126; Indels 3; Gaps 1;

QY 123 ACCACAGACGACCTCCACGCGTTGAGGGGCTTCCTGAGAACCTTAAGCGGCAAGAGGCGG 182
Db 359 AGCTCCACGCGCTCATGGCACTCAAGCGCGCCCTCGACCCCTCCGCGCGGGTCTCCACCT 418
QY 183 TCCGCTCCGCGCGGATGTCGCGGCGCTCATGCTGCAGCTGGAGAGGTGCGGATGCG 242
Db 419 CGTGTTCGCGCGCGGCGGACCCCTGCGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGG 478
QY 243 AACACAGCAAGCGCGCGGCTGCGGCGCTTCGCGGCTCCCGAACGCGCGCGGCGGATCA 302
Db 479 A---CGAGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 535
QY 303 TCCATGCTGATGTTGAGCTGTGATCACTTCGCTATTTGGATCTCTCGGGTAATTTCAT 362
Db 536 TCCCGCGGAGATCGCGCGGCTCGGAGCGCTGACCGGGCTGTACCTGCACTTCAACGCC 595
QY 363 TGGTTGGGAGGTACC 378
Db 596 TGGCGCGGAGGTGCC 611

RESULT 11
US-10-101-464A-865
; Sequence 865, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
```

```
; CURRENT APPLICATION NUMBER: US/10101464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 865
; LENGTH: 2735
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-101-464A-865

Query Match 3.9%; Score 38.4; DB 4; Length 2735;
Best Local Similarity 49.6%; Pred. No. 0.21;
Matches 127; Conservative 0; Mismatches 126; Indels 3; Gaps 1;

QY 123 ACCACAGACGACCTCCACGCGTTGAGGGGCTTCCTGAGAACCTTAAGCGGCAAGAGGCGG 182
Db 343 AGCTCCACGCGCTCATGGCACTCAAGCGCGCCCTCGACCCCTCCGCGCGGGTCTCCACCT 402
QY 183 TCCGCTCCGCGCGGATGTCGCGGCGCTCATGCTGCAGCTGGAGAGGTGCGGATGCG 242
Db 403 CGTGTTCGCGCGGCGGCGGACCCCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 462
QY 243 AACACAGCAAGCGCGCGGCTGCGGCGCTTCGCGGCTCCCGAACGCGCGGCGGCGGATCA 302
Db 463 A---CGAGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 519
QY 303 TCCATGCTGATGTTGAGCTGTGATCACTTCGCTATTTGGATCTCTCGGGTAATTTCAT 362
Db 520 TCCCGCGGAGATCGCGCGGCTCGGAGCGCTGACCGGGCTGTACCTGCACTTCAACGCC 579
QY 363 TGGTTGGGAGGTACC 378
Db 580 TGGCGCGGAGGTGCC 595

RESULT 12
US-09-228-986-39
; Sequence 39, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-228-986-39

Query Match 3.9%; Score 38.2; DB 3; Length 454;
Best Local Similarity 51.5%; Pred. No. 0.077;
Matches 88; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 217 CTGCACTCGGGAAGGTGCGGATGCGAAACAGCAAGCGCGCGCTCGTGGCGTTGGCGCT 276
Db 237 CTGCGCTGTGGAACGGAATTTCTGTCAGGCGCAACACAGAACGAGTGTGTTCAATTTCT 296
QY 277 CCCCAAGCGCGCTTGGAGGATCATCCATGCTGATGTTGGAGCTTGATCACTTCG 336
```

```
Db 297 CCTGAGTCTGTTGAATGATCGCTCTCCCGTATATTGGGAACCTCTCTCTTTGGG 356
Qy 337 CTATTGGATCTCTCGGTAATTCATTTGGTGGGAGGTACCAAAAGTTT 387
Db 357 GCATTTAGATCTTCTTCTGGAATGCTTTGAGTGGGAGAAATCCAGCAGATT 407

RESULT 13
US-10-101-464A-39
; Sequence 39, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgs, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/101,464A
; PRIORITY FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-101-464A-39

Query Match 3.9%; Score 38.2; DB 4; Length 454;
Best Local Similarity 51.5%; Pred. No. 0.077;
Matches 88; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 217 CTGAGCTGGGAGTGTGGGATGCGAAGACGAGCGCGCTGCGGTGGCGCT 276
Db 237 CTGCTGTGGAAACGGAATTTCTGTCAGGCCAAACACGAAACGAGTGGTTCAATTCTCT 296
Qy 277 CCCAAGCGCGCTTGGAGGATCATCCCATCGTCGATTTGGTGGTGTGATCACCCTTCG 336
Db 297 CCCTGAGTGTGTTGAATGATGCTCTCCCGTATATTGGGAACCTCTCTCTTTGGCG 356
Qy 337 CTATTGGATCTCTCGGTAATTCATTTGGTGGGAGGTACCAAAAGTTT 387
Db 357 GCATTTAGATCTTCTTCTGGAATGCTTTGAGTGGGAGAAATCCAGCAGATT 407

RESULT 14
US-10-101-464A-421
; Sequence 421, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgs, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/101,464A
; PRIORITY FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
```

```
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 421
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-101-464A-421

Query Match 3.9%; Score 38.2; DB 4; Length 498;
Best Local Similarity 51.5%; Pred. No. 0.081;
Matches 88; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 217 CTGAGCTGGGAGTGTGGGATGCGAAGACGAGCGCGCTGCGGTGGCGCT 276
Db 237 CTGCTGTGGAAACGGAATTTCTGTCAGGCCAAACACGAAACGAGTGGTTCAATTCTCT 296
Qy 277 CCCAAGCGCGCTTGGAGGATCATCCCATCGTCGATTTGGTGGTGTGATCACCCTTCG 336
Db 297 CCCTGAGTGTGTTGAATGATGCTCTCCCGTATATTGGGAACCTCTCTCTTTGGCG 356
Qy 337 CTATTGGATCTCTCGGTAATTCATTTGGTGGGAGGTACCAAAAGTTT 387
Db 357 GCATTTAGATCTTCTTCTGGAATGCTTTGAGTGGGAGAAATCCAGCAGATT 407

RESULT 15
US-09-621-976-15639
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15639
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15639

Query Match 3.9%; Score 38.2; DB 4; Length 505;
Best Local Similarity 12.3%; Pred. No. 0.082;
Matches 54; Conservative 188; Mismatches 196; Indels 1; Gaps 1;

Qy 184 CCGCTCCGCGCGCATGCTCCGCGCTCATCTGCGAGCTGGAAGTGTGGATCGGA 243
Db 6 SSRYTSSKSKRYGGKYSYSSRWSMKYAWGRKYGTSGRCGSGRGMWCKWGYRYSY 65
Qy 244 AACAGCAAGCGCGCGCTGCTGCGCTCCCCAAGCGCGCTTGGAGGATCAT 303
Db 66 WGYKWSKSKMKYSGKMGTSKS-TRKYTYTSKSKRTCKYRWSWKRWRKMY 124
Qy 304 CCATCGTGAATTTGGTGAATTCATCCCTTCGCTATTTGGATCTCTCGGTAATTCATT 363
Db 125 YRMYKVCYASYSYVRRCKRYTGMTRGWYCKRMCKSKSTRYMYTRYWMTGACYGS 184
Qy 364 GGTGGGAGGTACCAAAAGTTTGCAGATACCGCTCAAGAGCTCACCACTGACGCCA 423
Db 185 KGMSCGSRKSYGWSKRYGKTYTCTSKYKSMYSKYSKSMCTYMYMYCTY 244
Qy 424 GTCACTCGGTATGGTTCCATTAAACATGCTATTGCTGTGAGCAGTAGAAGACGCTCGA 483
Db 245 KSYTYTCKSKSYTYTSTKKGWGTKRSWSYTWMSKSYTWGSGSKKRWYWSAGAYAM 304
Qy 484 TGAAGAACCAATACATATACAGGACCAACAATAGTGTGGATCAGGGGACCAATGT 543
Db 305 MSWMCARMCMAMGMRSAWVKCSRAKMYMAKSCMYCAKMSCARSASAKGRCSCCTTKY 364
```


This Page Blank (uspro)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2005, 21:12:48 ; Search time 650 Seconds
(without alignments)
8925.148 Million cell updates/sec

Title: US-10-657-852A-3

Perfect score: 980

Sequence: 1 gcttgattccaatcaaggt.....ccctttacataaaaaaaaaa 980

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	980	100.0	980	ADM41460	Perennial
2	904.4	92.3	996	ADM41461	Adm41461 Tall fesc
3	541.6	55.3	1006	ADM41468	Adm41468 Tall fesc
4	503.6	51.4	1008	ADM41467	Adm41467 Perennial
5	492.8	50.3	1007	ADM41469	Adm41469 Perennial
6	451.2	46.0	1230	ADM41463	Adm41463 Tall fesc
7	443.6	45.3	1212	ADM41464	Adm41464 Perennial
8	421.8	43.0	1246	ADM41466	Adm41466 Tall fesc
9	419	42.8	1083	ADM41470	Adm41470 Perennial
10	417.4	42.6	1084	ADM41462	Adm41462 Perennial
11	394.4	40.2	1064	ADM41465	Adm41465 Perennial
12	270.4	27.6	959	ADM41459	Adm41459 Tall fesc
13	264.2	27.0	357	AAX99717	Aax99717 Grass ant
14	262.2	26.8	841	ADM41458	Adm41458 Perennial
15	79.4	8.1	4536	Adj40496	Adj40496 Plant cDN
16	54	5.5	2000	ADA71938	Ada71938 Rice gene
17	51.8	5.3	1138	AAN91630	Aan91630 3' sequen
18	50.6	5.2	1912	ADJ39568	Adj39568 Plant cDN
19	48.2	4.9	3000	ADI32615	Adi32615 Rice tran
20	44.8	4.6	3453	AAA79709	Aaa79709 Eucalyptu

c	21	43.8	4.5	235070	11	ACM45174	Acn45174 Human gen
	22	43	4.4	7722	3	AAA70168	Aaa70168 Plasmodiu
	23	41.6	4.2	2274	4	ABL17081	Ab117081 Drosophil
	24	41.6	4.2	4274	4	ABL17080	Ab117080 Drosophil
c	25	41.4	4.2	966	6	ABQ17272	Abq17272 Oligonuc1
	26	41.4	4.2	966	6	ABQ17273	Abq17273 Oligonuc1
	27	41	4.2	408	3	AAA79411	Aaa79411 Eucalyptu
c	28	40.8	4.2	702	5	AAS67541	Aas67541 DNA encod
	29	40.4	4.1	396	3	AAA79420	Aaa79420 Eucalyptu
	30	40.4	4.1	3381	2	AAV41343	Aav41343 M. catarr
c	31	40.4	4.1	12614	4	AAI99322	Aai99322 Human exc
	32	40.4	4.1	12614	5	AAI63672	Aai63672 Human kid
c	33	40.2	4.1	3228	5	AAS81183	Aas81183 DNA encod
	34	40	4.1	804	12	ADM80069	Adm80069 Spiramyci
c	35	40	4.1	804	12	ADN97585	Adn97585 S ambofac
	36	40	4.1	30943	12	ADM80034	Adm80034 Spiramyci
c	37	40	4.1	30943	12	ADN97550	Adn97550 S ambofac
	38	39.6	4.0	2000	8	ADA71938	Ada71938 Rice gene
c	39	39.6	4.0	2298	4	ABL18481	Ab118481 Drosophil
	40	39.6	4.0	2479	11	ADM03281	Adm03281 Human cDN
	41	39.6	4.0	4298	4	ABL18480	Ab118480 Drosophil
	42	39.2	4.0	1443	10	ABZ23668	Abz23668 H. pylori
c	43	39.2	4.0	2274	4	ABL17081	Ab117081 Drosophil
	44	39.2	4.0	4274	4	ABL17080	Ab117080 Drosophil
c	45	38.8	4.0	1028	3	AAA50251	Aaa50251 Maize hea

ALIGNMENTS

RESULT 1
ADM41460
ID ADM41460 standard; cDNA; 980 BP.
XX
AC ADM41460;
DT 03-JUN-2004 (first entry)
XX
DE Perennial ryegrass antifreeze protein AFP2 cDNA.
XX
KW Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;
KW antigout; litholytic; nephrotropic; cytostatic; gene; ss.
XX
OS Lolium perenne.
FH Key Location/Qualifiers
FT CDS 35..838
FT /*tag= b
FT /*product= "Antifreeze protein AFP2"
FT sig_peptide 35..103
FT /*tag= a
FT mat_peptide 104..835
FT /*tag= c

WO2004022700-A2.

18-MAR-2004.

09-SEP-2003; 2003WO-NZ000199.

09-SEP-2002; 2002US-0409557P.

(GENE-) GENESIS RES & DEV CORP LTD.

(WRIG-) WRIGHTSON SEEDS LTD.

Demmer J, Sherk MA, Hall C, Fish SA;

WPI: 2004-248453/23.

P-PSDB; ADM41473.

XX New antifreeze proteins and encoding polynucleotides, useful for
PT modulating cold tolerance in organisms, as food additives, or for
PT treating tumors or disorders associated with the presence of unwanted

PT biocrystals (e.g. gout).

XX Claim 1; SEQ ID NO 3; 71pp; English.

XX The present sequence is that of cDNA encoding APP2, an antifreeze protein

CC of perennial ryegrass. The cDNA was isolated from a leaf blade cDNA

CC expression library. The invention provides forage grass (perennial

CC ryegrass and tall fescue) antifreeze proteins and the polynucleotides

CC encoding them ADM41458-ADM41483. The polynucleotides were isolated from

CC tissues taken at different times of year (winter and spring) and from

CC different parts of the plants. The polynucleotides can be used to

CC modulate the cold tolerance of an organism, especially plants, mammals,

CC insects, fungi, archaea and bacteria. The method involves incorporating

CC an antifreeze polynucleotide, under the control of a gene promoter

CC sequence, into the genome of the organism, or introducing double-stranded

CC RNA corresponding to the polynucleotide into the cells of the organism,

CC thereby inhibiting expression of an antifreeze polypeptide. The

CC antifreeze protein can be used for the cryopreservation of a cell or

CC tissue, as a food additive of a frozen food product, in a method for

CC decreasing the time required to dehydrate a composition, to treat a

CC disorder characterised by biocrystals associated with disorders such as

CC gout and kidney stones, to preserve the viability of a molecular biology

CC reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and

CC to protect a plant from damage due to frost or freezing.

XX Sequence 980 BP; 264 A; 223 C; 253 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 980; DB 12; Length 980;

Best Local Similarity 100.0%; Pred. No. 9e-297;

Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGCAATCAATCAAGGTTCTTGTTCAATCATGCTCAATACATGGCAAGTGTG 60

DB 1 GCTTGCAATCAATCAAGGTTCTTGTTCAATCATGCTCAATACATGGCAAGTGTG 60

QY 61 CATGCTGCTGTTCTTTGGGTTTCATCTTCAGGTGGCAGGCAACGTCGTGTCGTG 120

DB 61 CATGCTGCTGTTCTTTGGGTTTCATCTTCAGGTGGCAGGCAACGTCGTGTCGTG 120

QY 121 CCACACAGACCTCCACGGTTGAGGGGCTGCTGAGAACCTTAAGCGGCAAGGAGC 180

DB 121 CCACACAGACCTCCACGGTTGAGGGGCTGCTGAGAACCTTAAGCGGCAAGGAGC 180

QY 181 CGTCCGCTCCGCGCGCATGCTCGCGGCTCATGCTGCAGCTGGGAAGTGGGATG 240

DB 181 CGTCCGCTCCGCGCGCATGCTCGCGGCTCATGCTGCAGCTGGGAAGTGGGATG 240

QY 241 CGAAACAGACAGCGCGCGCTGCGGCTTCCGCTCCCAAGCGCGGCTTGGAGGAT 300

DB 241 CGAAACAGACAGCGCGCGCTGCGGCTTCCGCTCCCAAGCGCGGCTTGGAGGAT 300

QY 301 CATCCATGCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 360

DB 301 CATCCATGCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 360

QY 361 ATTGTTGGGAGGTACCAAAAGTTTCAGATAGGCTCAAGAGCTCACCCTGACAG 420

DB 361 ATTGTTGGGAGGTACCAAAAGTTTCAGATAGGCTCAAGAGCTCACCCTGACAG 420

QY 421 CCAGTCACTCGGTATGGTTCATTAACATGCTATTGATGATGATGATGATGATGATG 480

DB 421 CCAGTCACTCGGTATGGTTCATTAACATGCTATTGATGATGATGATGATGATGATG 480

QY 481 CGATGAGAACCAATACAAATATCAGGACCAACAAATAGTGTGATCAGGAGCAACAA 540

DB 481 CGATGAGAACCAATACAAATATCAGGACCAACAAATAGTGTGATCAGGAGCAACAA 540

QY 541 TGTGTTTCCGGGATGACACACGCTGCTATCTGGGAATAACAACTGCTCTGGGAG 600

DB 541 TGTGTTTCCGGGATGACACACGCTGCTATCTGGGAATAACAACTGCTCTGGGAG 600

QY 601 CAACAACACTGTTGTAATGGAAGTGACAAATGATGATGATGATGATGATGATGATG 660

DB 601 CAACAACACTGTTGTAATGGAAGTGACAAATGATGATGATGATGATGATGATGATG 660

Db 601 CAACAACACTGTTGTAATGGAAGTGACAAATGATGATGATGATGATGATGATGATG 660

QY 661 AGGACAAAGCATATTTGTTACTGATAACAATAATGTTGTTATCCGGGAACGACAATATGT 720

Db 661 AGGACAAAGCATATTTGTTACTGATAACAATAATGTTGTTATCCGGGAACGACAATATGT 720

QY 721 GTCTGGAAGCTTCCATCTACTGATCAGGGGACCAATACCGTATCCGGGACCAACATAC 780

Db 721 GTCTGGAAGCTTCCATCTACTGATCAGGGGACCAATACCGTATCCGGGACCAACATAC 780

QY 781 TGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAAACAGATGGTTAATA 840

Db 781 TGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAAACAGATGGTTAATA 840

QY 841 TTCTGTAGTGCAGGATGCTTCCATCTTCCAAAGTTCAGTGTAGCTTACAAATAGA 900

Db 841 TTCTGTAGTGCAGGATGCTTCCATCTTCCAAAGTTCAGTGTAGCTTACAAATAGA 900

QY 901 TGGAGACAATCACGTTATGTAACCTTCAGGATATGCAATCTTTCCTTTAAATAAGCTT 960

Db 901 TGGAGACAATCACGTTATGTAACCTTCAGGATATGCAATCTTTCCTTTAAATAAGCTT 960

QY 961 CCCTTTACATAAAAAAAA 980

Db 961 CCCTTTACATAAAAAAAA 980

RESULT 2

ADM41461

ID ADM41461 standard; cDNA; 996 BP.

XX ADM41461;

XX 03-JUN-2004 (first entry)

XX Tall fescue antifreeze protein cDNA.

DE Antifreeze; fescue; cold tolerance; transgenic; plant; antigout;

KW litholytic; nephrotropic; cytostatic; gene; ss.

XX Schedonorus arundinaceus.

XX Key Location/Qualifiers

FT CDS 41..850

FT /*tag= b

FT /product= "Antifreeze protein"

FT /transl_except= (pos:410..412,aa:Xaa)

FT /note= "Xaa= unknown"

FT sig_peptide 41..112

FT /*tag= a

FT mat_peptide 113..847

FT /*tag= c

XX WO2004022700-A2.

XX 18-MAR-2004.

XX 09-SEP-2003; 2003WO-NZ000199.

XX 09-SEP-2002; 2002US-0409557P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (WRIG-) WRIGHTSON SEEDS LTD.

XX Demmer J, Shenk MA, Hall C, Fish SA;

XX WPI; 2004-248453/23.

XX P-PSDB; ADM41474.

XX New antifreeze proteins and encoding polynucleotides, useful for

XX modulating cold tolerance in organisms, as food additives, or for

XX treating tumors or disorders associated with the presence of unwanted

XX biocrystals (e.g. gout).

Claim 1; SEQ ID NO 4; 71pp; English.

The present sequence is that of cDNA encoding an antifreeze protein of tall fescue. The cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them (ADN41458-ADN41483). The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to frost or freezing.

Sequence 996 BP; 268 A; 235 C; 250 G; 243 T; 0 U; 0 Other;

Query Match	92.3%;	Score	904.4;	DB	12;	Length	996;
Best Local Similarity	96.2%;	Pred. No.	5.2e-273;				
Matches	949;	Conservative	0;	Mismatches	31;	Indels	6;
Gaps	2;						

Qy	1	GCTTGCATTCGAATCAAGGTTCTTGTTCAATCCATGCTGAATACATGGCAAAGTGTG	60
Dd	7	GCTTGCATTCGAATCAAGGTTCTTGTTCAATCCATGCTGAATACATGGCAAAGTGTG	66
Qy	61	CATGCTGCTGCTCTCTTGGGTTCA--TCATTGAGGTGGCAGCAGCAAGTGTGTC	117
Dd	67	CATGCTGCTGCTCTCTTGGGTTCACTCTTTCAGGTGGCGGAGCAAGTGTGTC	126
Qy	118	GTGCCACCAGCAGCACCTCCACCGTGTGAGGGGCTCGCTGAGAACCCTAAGCGCAAGG	177
Dd	127	GTGCCACCAGCAGCACCTCCGCGCATTTAGGGGCTTCGCCGAGAACCTAAGCGCAAGG	186
Qy	178	AGCGTCCGCTCCGCGCGCATGFTCCGGCGCTCATGCTGCAGCTGGGAAGTGTGG	237
Dd	187	AGCGTCCGCTCCGCGCGCATGFTCCGGCGCTCATGCTGCAGCTGGGAAGTGTGG	246
Qy	238	ATGCGAACAAGCAGCGCGCTGCTGGCGGTTCGGCTCCCAGCGCGCTTGGAGG	297
Dd	247	ATGCGAACAAGCAGCGCGCTGCTGGCGGTTCGGCTCCCAGCGCGCTTGGAGG	306
Qy	298	GATCATCCCATCTCGATTGGTGCAGCTTCATCACCTTCGTTATTTGGATCTCTCGGGTAA	357
Dd	307	GACATCCCATCTCGATTGGTGCAGCTTCATCACCTTCGTTATTTGGATCTCTCGGGTAA	366
Qy	358	TTCATTGGTTGGGAGGTACCAAAAAGTTTGCAGATACCGGCTCAAGAGCCTCACCACTGA	417
Dd	367	TTCATTGGTTGGGAGGTACCAAAAAGTTTGCAGATACCGGCTCTAGAGCCTCTCCACTGA	426
Qy	418	CAGCAGTCACTCGGTATGGGTTGCATTAACATGCTATTGCTATGACAGT---AGAG	474
Dd	427	TGGCAGTCACTCGGTATGGGTTGCATTAACATGCTATTGCTATGACAGTAAACAGAG	486
Qy	475	AAGCTCGATGAGAACCAATAATATATCAGGACCAACAATAGTTGGATCAGGAG	534
Dd	487	AACCTCGATGAGAACCAATAATATATCAGGACCAACAATAGTTGGATCAGGAG	546
Qy	535	CAACAATGTTGTTTCCGGGAATGACCAACGCGTGTATCTGGGAATAACAACATGTGTC	594
Dd	547	CAACAATGTTGTTTCCGGGAATGACCAACGCGTGTATCTGGGAATAACAACATGTGTC	606
Qy	595	TGGGAGCAACAACATCTGTTAACTGGAATGACAAATCTGTAGTTGGTAGCAACATGT	654
Dd	607	TGGGAGCAACAACATCTGTTAACTGGAATGACAAATCTGTAGTTGGTAGCAACATGT	666

Qy	655	CGTATCAGGACAAAGCATATTTACTGATAACAATAATGTTTCTATCCGGGACGACAA	714
Dd	667	CGTATCAGGACAAAGCATATTTACTGATAACAATAATGTTTCTATCCGGGACGACAA	726
Qy	715	TAAATGCTCTGGAAGCTTCCATCTGATCAGGGGAGCACAATACCGTATCCGGGAGCAA	774
Dd	727	TAAATGCTCTGGAAGCTTCCATCTGATCAGGGGAGCACAATACCGTATCTGGGAGCAA	786
Qy	775	CAATAGTCTATCCGGGAGCAACCATATCTGATCTGGGAGCAACAAGTCTGTAACAGATGG	834
Dd	787	CAACACTGATCCGGGAGCAACCATATCTGATCTGGGAGCAACAAGTCTGTAACAGATGG	846
Qy	835	TAAATATCTGATGTCAGGATTCGCTTCATCTCTCCCAAGTTCAGTGTAGCTTCAATC	894
Dd	847	TAAATATCTGATGTCAGGATTCGCTTCATCTCTCCCAAGTTCAGTGTAGCTTCAATC	906
Qy	895	AATAGATGAGACAAATCAGTTCATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT	954
Dd	907	AATAGATGAGACAAATCAGTTCATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT	966
Qy	955	AAGCTTCCCTTTACATAAAAAAAA 980	
Dd	967	AAGCTTCCCTTTACATAAAAAAAA 992	

RESULT 3	
ID	ADM41468
XX	ADM41468 standard; cDNA; 1006 BP.
AC	ADM41468;
XX	
DT	03-JUN-2004 (first entry)
XX	
DE	Tall fescue antifreeze protein cDNA.
XX	
KW	Antifreeze; fescue; cold tolerance; transgenic; plant; antigout;
XX	litholytic; nephrotropic; cytotstatic; gene; ss.
OS	Schedonorus arundinaceus.
XX	
PH	Key Location/Qualifiers
FT	CDS 53..841
FT	/tag= b
FT	/product= "Antifreeze protein"
FT	sig_peptide 53..121
FT	/tag= a
FT	mat_peptide 122..838
FT	/tag= c
XX	
PN	WO2004022700-A2.
XX	
PD	18-MAR-2004.
XX	
PF	09-SEP-2003; 2003WO-NZ000199.
XX	
PR	09-SEP-2002; 2002US-0409557P.
XX	
PA	(GENE-) GENESIS RES & DEV CORP LTD.
PA	(WRIG-) WRIGHTSON SEEDS LTD.
XX	
PI	Demmer J, Shenk MA, Hall C, Fish SA;
XX	
DR	WPI; 2004-248453/23.
DR	P-PSDB; ADM41481.
XX	
XX	New antifreeze proteins and encoding polynucleotides, useful for
PT	modulating cold tolerance in organisms, as food additives, or for
PT	treating tumors or disorders associated with the presence of unwanted
PT	biocrystals (e.g. gout).
XX	
PS	Claim 1; SEQ ID NO 11; 71pp; English.
XX	

CC The present sequence is that of cDNA encoding an antifreeze protein of
 CC tall fescue. The cDNA was isolated from a leaf blade cDNA expression
 CC library. The invention provides forage grass (perennial ryegrass and tall
 CC fescue) antifreeze proteins and the polynucleotides encoding them
 CC ADM41458-ADM41483. The polynucleotides were isolated from tissues taken
 CC at different times of year (winter and spring) and from different parts
 CC of the plants. The polynucleotides can be used to modulate the cold
 CC tolerance of an organism, especially plants, mammals, insects, fungi,
 CC archaea and bacteria. The method involves incorporating an antifreeze
 CC polynucleotide, under the control of a gene promoter sequence, into the
 CC genome of the organism, or introducing double-stranded RNA corresponding
 CC to the polynucleotide into the cells of the organism, thereby inhibiting
 CC expression of an antifreeze polypeptide. The antifreeze protein can be
 CC used for the cryopreservation of a cell or tissue, as a food additive of
 CC a frozen food product, in a method for decreasing the time required to
 CC dehydrate a composition, to treat a disorder characterised by biocrystals
 CC associated with disorders such as gout and kidney stones, to preserve the
 CC viability of a molecular biology reagent, to destroy unwanted tissue in a
 CC patient e.g. tumour tissue, and to protect a plant from damage due to
 CC frost or freezing.

SX Sequence 1006 BP; 248 A; 261 C; 260 G; 237 T; 0 U; 0 Other;

Query Match 55.3%; Score 541.6; DB 12; Length 1006;

Best Local Similarity 76.5%; Pred. No. 5.3e-159;

Matches 756; Conservative 0; Mismatches 194; Indels 38; Gaps 6;

QY 22 TCTTCTTCAATCATGCTGATATCATGCAAGTGTTCATGCTGCTGCTCTTCTGGG 81
 DB |||||
 DB 28 TCTATAGCATAGCATGCTGTAATCATGCGGAATGCTTGATGCTGCTCTCTCTCGC 87
 QY 82 GTTCATCTTGACAGGTGGCAGGA--GCAACGTCGTGTCGTGCCACACGACGACTCCA 138
 DB |||||
 DB 88 GTTCTCTTGTGCGGGCTTGCACGCGCAGCGGCGCATGCCACCGGGATGACTCCG 147
 QY 139 CGCGTTGAGGGCTCTGCTGAGAACTTAAGGGGCAAGAGCGGTCGCCCTCCGCGCGC 198
 DB |||||
 DB 148 TCGCTGCGGGGCTTTCGCTGAGAACTGCGGGCGCGCGCACTCAGCCTTCGCGCGC 207
 QY 199 ATGTCGCGGCGCTCATGCTCAGCTGGAGAGGTGTGGATGCGAAGCAGCAAGCGCGC 258
 DB |||||
 DB 208 GTGGTCAGCGGCTCATGCTGCGATTTGGAGAGCGCTTGGCTGCGACGGTGGCAGCGCGC 267
 QY 259 CGTCGTGGCGTTGCGGCTCCCAAGCGCGGCTTGGAGGGATCATCCCATCTGTCGATTGG 318
 DB |||||
 DB 268 TGTACGCGCTTGTGCTCTCCAGGAGCGGCTCAGCGGGCCATCCCATCTGTCGATTG 327
 QY 319 TGAGCTTGATCACCTTTCGCTATTGGATCTCTCGGGTAATTCATTGGTTGGGAGGTACC 378
 DB |||||
 DB 328 TCAGCTTCACCACTTACGCTACTTGGATCTTTTCAGGTAATGCTGTTGGCGAGGTACC 387
 QY 379 AAAAAGTTTGAGATACGCGCTCAGAGCCTCACCACCTCAGAGCCAGTCACTCGGTATGGG 438
 DB |||||
 DB 388 CAAGAACTGACAGGTACAGCTCAAGAGGCTCACCGCTCCCGGTC-----GTTGGG 438
 QY 439 TTCCATTAACTGCTATTGCTGTGA---GCAGTAGAGAAAGCGTCCGATGAAGAACCAA 495
 DB |||||
 DB 439 TTTACCAACATGCAATTCATGATGATGCTGTAAAGAGATCACTCGAGCAGAGCCCAA 498
 QY 496 TACAATATCAGGAGCAACAATAGTTGGATTCAGGAGCAACAATGTTGTTTCGGGAA 555
 DB |||||
 DB 499 TACAATATCTGGAGCAACAATCTGTCAGATCCGGAGCAAAAATGTTGTTGCTGGAA 558
 QY 556 TGACAACACGTCGATCTGGGATAACAACCTGTCCTGGAGCAACACACTGTTGT 615
 DB |||||
 DB 559 TGACAACACGTCATATCTGGGACACAATAGTGTGTCGGAGCAACAACACTGTCGT 618
 QY 616 AACTGGAAGTGACATATCTAGTTGGTAGCAACCATGTCGTATCAGGAGCAAAAGCATAT 675
 DB |||||
 DB 619 AAGTGGGAGTGACAATACCGTAACCTGGCAGCAACCATCTGTCATCAGGAGCAACACATAT 678
 QY 676 TGTTACTGATACAAATATGTTGATCTCGGGAACGACAATATGTTGTCGGAAGTCTCCA 735
 DB |||||

DB 679 CGTTACAGACAAACAATAACGTTATCCGGAGACGATAATATGTTATCCGGAGCTTTCA 738
 QY 736 TACTGTATCAGGGAGGACATACGTTATCCGGAGGCAACAATATGTTATCCGGAGCAA 795
 DB |||||
 DB 739 TACCGTATCCGGGGGACAAATACCGTCTCTGGGAGCAACAATACCGTATCTGGGAGCAA 798
 QY 796 CCATATCGTATCTCGGAGCAACAAGTCTGAACAGATGGTTAATATTTCTGTAGTGCAGG 855
 DB |||||
 DB 799 CCAATGTTGATCTCGAAGCAACAAGTCTGCACAGCGCTTAATCACTGTCAGCGCATG 858
 QY 856 ATTGCTTCCACTTT-----CCCAAGTTCAGTGTAGCTTCAATCAA 896
 DB |||||
 DB 859 ATTGTTTCCACTTAACTGAGCTCAGCTTCTTGTCCCAAGTTCACTGTACCTCACAGTCAG 918
 QY 897 TAGATGGAGCAATCAGTTATGTAACCTCA-GGATATGGCATACTTTTC---CTTTAAA 952
 DB |||||
 DB 919 TTGTGCGTTCAATCGCGGTATGTAATTCATGATATACCATACTTTTCTCTACTATATA 978
 QY 953 TAAAGCTTCCCTTTCACATAAAAAAAA 980
 DB |||||
 DB 979 TAAATTTCCCTTAAAAAAA 1006

RESULT 4

ADM41467

ID ADM41467 standard; cDNA; 1008 BP.

XX AC ADM41467;

DT 03-JUN-2004 (first entry)

DE Perennial ryegrass antifreeze protein APP5 cDNA.

KW Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;
 KW antigout; litholytic; nephrotropic; cytostatic; gene; ss.

OS Lolium perenne.

FH Key Location/Qualifiers

FT CDS 79..843

FT /*tag= b

FT /product= "Antifreeze protein APP5"

FT sig_peptide 79..147

FT /*tag= a

FT mat_peptide 148..840

FT /*tag= c

XX WO2004022700-A2.

PN 18-MAR-2004.

XX 09-SEP-2003; 2003WO-NZ000199.

XX 09-SEP-2002; 2002US-0409557P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (WRIGHTSON SEEDS LTD.

XX Demmer J, Shenk MA, Hall C, Fish SA;

XX WPI; 2004-248453/23.

XX P-PSDB; ADM41480.

XX New antifreeze proteins and encoding polynucleotides, useful for
 XX modulating cold tolerance in organisms, as food additives, or for
 XX treating tumors or disorders associated with the presence of unwanted
 XX biocrystals (e.g. gout).

XX Claim 1; SEQ ID NO 10; 71pp; English.

XX The present sequence is that of cDNA encoding APP5, an antifreeze protein
 XX of perennial ryegrass. The cDNA was isolated from a leaf blade cDNA
 XX expression library. The invention provides forage grass (perennial

ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them ADM41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to frost or freezing.

XX Sequence 1008 BP; 256 A; 265 C; 251 G; 236 T; 0 U; 0 Other;

Query Match 51.4%; Score 503.6; DB 12; Length 1008;
 Best Local Similarity 74.3%; Pred. No. 4.7e-147;
 Matches 742; Conservative 0; Mismatches 194; Indels 62; Gaps 6;

QY 12 AATCAGGTTTCTTGTTCATCATGCTGCAATACATGGCAAAAGTTGTGATGCTGCTGG 71
 DB 44 ATTGAATCCATATATAGCATAGCACTGCTGAATCCATGGCGAAATGCTTGTGCTGTC 103
 QY 72 TCTTCTGGGGTTCATCTTCAGTGGGAGCA--GCAAGCTGCTGCTGCTGCGCACACG 128
 DB 104 TCTCTTGGGTTCTTGTGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 163
 QY 129 ACGACCTCCACGCGGCTTGAGGGGCTGCTGCTGAGAACCTTAAGCGGCAAGAGCGGCTCGGCC 188
 DB 164 ATGACCTTCGCGGCTGCGGGGCTTCGCTGAGAACCTTGGCGGCGGCGGCGGCGGCGG 223
 QY 189 TCGCGCGCGGATGCTGCGGCGCTCATGCTGAGCTGGGAAGTGTGGGATGCGAAACAG 248
 DB 224 TCGCGCGCGGCTGCTGAGGGGCTCATGCTGCGATTTGGGAAGGCTTGGCTGCGGCGGTG 283
 QY 249 CAGCGCGCGGCTGCTGCGGCTTGGGCTCCGAGCGGCGGCTTGGAGGATCATCCCAT 308
 DB 284 CCAGCGCGGCTGCTGCGGCTTGGGCTCCGAGCGGCGGCTTGGAGGATCATCCCAT 343
 QY 309 CGTGCATTTGCTGAGCTGATCAGCTTCTGATTTGATCTCTCGGGTAATTCATTTGTTG 368
 DB 344 CATGATTTGCTGAGCTTACCACTAGCTACTTGGATCTTTCAGTAAATGATTTGGTTG 403
 QY 369 GGGAGGTACCAAAAGTTTGCAGATACGCTGCAAGAGCCTTCACTGACGCGAGTCA 428
 DB 404 GCGAGGTACCAAGATCTGAGGTACAGCTCAAGGATCACC----- 447
 QY 429 TCGGTATGGTTTCCATTAATGCTATTTGATGTA---CGAGTAGAGAACGCTGATG 485
 DB 448 -----AACATGCCATTTGATGATGCTGATGCGTAAACAGAGATCACTGACG 490
 QY 486 AAGAACCAATACAAATACAGGACCAACAATAGTTGATCAGGAGCAACAATGTTG 545
 DB 491 AGCAGCCCAATACAAATTTCTGGGAGCAACAATCTGTCAGATCCGGAGCAAAATGTTT 550
 QY 546 TTTCGGGAATGACCAACAGGTCGTATCTGGGAATACCAACCATGTTCTGGGAGCAACA 605
 DB 551 TTGCTGGGAATGACCAACAGGTCGTATCTGGGAGCAACAATGTTCTGGGAGCAACA 610
 QY 606 AACTGTTGTAATGGAAGTGACAATCTGATTTGTTAGCAACCATGCTGTATCAGGGA 665
 DB 611 AACTGTTGTAATGGAAGTGACAATCTGATTTGTTAGCAACCATGCTGTATCAGGGA 670
 QY 666 CAAGCATATTTGTTACTGATAACAATATGTTGTTCTGGGAGCAACAATGTTGTTCTG 725
 DB 671 CAACCATATCTGTTACAGCAACAACAATACGTTATCCGGGAGCAACAATGTTATCCG 730
 QY 726 GAAGCTTCCATCTGTTATCAGGGAGCAACAATACCGGTATCCGGGAGCAACAATCTGAT 785

DB 731 GGAGCTTTTCATACCGTATCCGGGGGCAAAATCTGTCTCCGGAGCAACAATACCGTAT 790
 QY 786 CCGGAGCAACCATATCTGATCTGCGGAGCAACAAGTCTGTAACAGATGTTAATATCTG 845
 DB 791 CTGGGAGCAACCATGTTGATCTGGAAGCAACAAGTCTGTAACAGATGTTAATATCTG 850
 QY 846 TAGTCTGAGGATGTTCTCCATCTT-----CCCAAGTTCAAGTGTAGC 886
 DB 851 TCAGCGCATGATTTGTTTCCACCTTAATCTGAGCTCAGCTTCTTCCCAAGTTCACTGTACC 910
 QY 887 TTACATCAATAGATGCGAGCAATCACTGATTAATCTTCA--GGATATGCGCATCTTTC 945
 DB 911 TCACAGTCTGTTGCTGCTTCAATCGGTTATGTAATCTTCAATGATATACCATCTTTC 970
 QY 946 ---CTTTAATAAAGCTTCCCTTTACATAAAAAAAA 980
 DB 971 CTACTATATAAATAATTTCCCTTTACATAAAAAAAA 1008

RESULT 5
 ADM41469
 ID ADM41469 standard; cDNA; 1007 BP.
 XX ADM41469;
 DT 03-JUN-2004 (first entry)
 DE Perennial ryegrass antifreeze protein cDNA.
 XX Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;
 KW antigout; litholytic; nephrotropic; cytostatic; gene; ss.
 XX Lolium perenne.
 FH Key Location/Qualifiers
 CDS 72..842
 /tag= b
 /product= "Antifreeze protein"
 sig_peptide 72..140
 /tag= a
 mat_peptide 141..839
 /tag= c
 WO2004022700-A2.
 18-MAR-2004.
 09-SEP-2003; 2003WO-NZ000199.
 09-SEP-2002; 2002US-0409557P.
 (GENE-) GENESIS RES & DEV CORP LTD.
 (WRIG-) WRIGHTSON SEEDS LTD.
 Demmer J, Shenk MA, Hall C, Fish SA;
 WPI: 2004-248453/23.
 P-PSDB; ADM41482.
 New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted biocrystals (e.g. gout).
 Claim 1; SEQ ID NO 12; 71pp; English.
 The present sequence is that of cDNA encoding, an antifreeze protein of perennial ryegrass. The cDNA was isolated from a leaf and pseudostem cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them ADM41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from

CC viability of a molecular biology reagent, to destroy unwanted tissue in a
CC patient e.g. tumour tissue, and to protect a plant from damage due to
CC frost or freezing.

XX SQ Sequence 1246 BP; 313 A; 294 C; 307 G; 332 T; 0 U; 0 Other;

Query Match 43.08; Score 421.8; DB 12; Length 1246;
Best Local Similarity 70.18; Pred. No. 2.7e-121;
Matches 690; Conservative 0; Mismatches 192; Indels 103; Gaps 5;

QY 63 TGTCTGCTGCTCTCTTCTGGGTTTCATCTTGCAGGTGGCGAGGCAACGTCGTGTCGTGCC 122
DB 60 TGTCTGCTGCTCTCTTCTGGGTTTCATCTTGCAGGTGGCGAGGCAACGTCGTGTCGTGCC 119
QY 123 ACCACGACGACCTCCACGCGTTGAGGGCCCTCGCTGAGAACCTAAAGCGCAAGAGGCGCG 182
DB 120 ACCCGATGACCTCCGTCGCTCGGGGCTTTGCCAAGACGTTGGTGC---GGAGCG 176
QY 183 TCGGCTCCGGCGCGCAGTGTGGCGCCTCATCTGCTGACGTGGGAAGGTGTGGATGCG 242
DB 177 TCTCTCTCCGCGACGCGTGTGGCGACCTCGTCTGCGTCTGGAAGGTGTGGATGCA 236
QY 243 AAACAGCAAGCGCGCGTGTGGCGTGGCGTCCCGAGCGCGCTTGGAGG--- 298
DB 237 ATGGCGGAGCGCGCATCACACGTTGTGGCTTCCCTAGCGGTGGCTTGGCGGGACCA 296
QY 299 ----- 298
DB 297 TCACAGGAGCATCTTGGCGGCTCGGAGGCTGGAGTCACCTCAACCTTGCCACACACA 356
QY 299 -----ATCATCCCATCGTCGATTCGGTGGTGTGATCATCTTCGCTATTTGGATC 347
DB 357 GACTGTGGCGCACCATCCATCGTGGATTCGTGAGCTTGACCACTTCTCTACTTGGATC 416
QY 348 TCTCGGTAATTCATTTGGTGGGAGGTACCAAAAGTTTGCAGATACGCTCAAGGCC 407
DB 417 TCTCACATAATTCATTTGGTGGGAGCTGCCAACCGTTTGCAGATACGCTCAAGGCC 476
QY 408 TCACCACTGACAGCGAGTCTCGTATGGTTCATTAACATGCTATTCATGTGA--- 464
DB 477 TCACCAACAGGTCTATTTAGTATGCTTTCATTAACATGCTATTCATGTGAGC 536
QY 465 GCATGAGAAGCGCTCGATGAGAACAACAAATATATCAGGAGCAACAATAGTGTG 524
DB 537 GTAACAGAAGAACTCTCGCCATACAAACAAATATATCTGGAGCAACAATCTGTCT 596
QY 525 GATCAGGAGCAACAATGTTTTCGGGATGACACACGCTGATCTGGGAATACA 584
DB 597 TATCTGGGCGAAACAATGTTTCTGGGAATGACACACCTGTATATCGGAGACACA 656
QY 585 ACCATGTCTGGGAGCAACAACACTCTGTGAAGTGAACAATCTGTAGTTGGTA 644
DB 657 ATACTGTCTGTAGTCTCAACACCGTCAACCGGAGTGAACAATCTTAACTGGGA 716
QY 645 GCAACCATGTCTATCAGGAGCAACAATATTTACTGATAACAATATGTTGATCCG 704
DB 717 GCAACCATGTCTATCAGGAGCAACAATATTTACTGATAACAATATGTTGATCTG 776
QY 705 GGAACGCAATAATGTTCTGGAAGCTTCACTATGATCAGGGAGCAACAATACGTTAT 764
DB 777 GGAACGCAATAATGTTCTGGGAGCTTCCATAAAGTATCCGGAAGTCAACAATACGTTAT 836
QY 765 CCGGAGCAACAATCTATCAGGAGCAACAATATCTGATCTGGGAGCAACAATAGTCG 824
DB 837 CTGGAGCAACAATACCGTATCGGGAGAACCAATGCTGATCTGGGAGCAACAATATCG 896
QY 825 TAACAGATGTTAATATTTCTGTAGGTGCA-----GGATGTCTTC 864
DB 897 TGACAGGAGTTAATGATATGTTAGTGTGTTTCCATCTTCCTAAGGATCTCAGT 956
QY 865 ATCTTCCCAAGTTTCAGTGTAGCTTACAATCAATAGATGGAGACAATCACTTATGTA 924
DB 957 ACTTGACAGATTCAGTGTAGCTCAATCACTTGTGGGAGCAACAATCGGTTATGTA 1016

QY 925 TCA--GGATATGGCATACTTTCTCT 947
DB 1017 TCATGGATATATCATACCTTTCTCT 1041

RESULT 9
ADM41470
ID ADM41470 standard; cDNA; 1083 BP.
XX ADM41470;
AC ADM41470;
XX 03-JUN-2004 (first entry)
XX Perennial ryegrass antifreeze protein cDNA.
DE Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;
KW antitox; litholytic; nephrotropic; cytostatic; gene; ss.
XX Lolium perenne.
FH Key Location/Qualifiers
CDS 59..904
FT /tag= b
FT /product= "Antifreeze protein"
FT sig_peptide 59..115
FT /tag= a
FT mat_peptide 116..901
FT /tag= c
XX WO2004022700-A2.
PN 18-MAR-2004.
XX 09-SEP-2003; 2003WO-NZ000199.
XX 09-SEP-2002; 2002US-0409557P.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX (WRIG-) WRIGHTSON SEEDS LTD.
XX Demmer J, Shenk MA, Hall C, Fish SA;
XX WPI; 2004-248453/23.
XX P-PSDB; ADM41483.

XX New antifreeze proteins and encoding polynucleotides, useful for
PT modulating cold tolerance in organisms, as food additives, or for
PT treating tumors or disorders associated with the presence of unwanted
PT biocrystals (e.g. gout).

XX Claim 1; SEQ ID NO 13; 71pp; English.

XX The present sequence is that of cDNA encoding, an antifreeze protein of
CC perennial ryegrass. The invention provides forage grass (perennial
CC ryegrass and tall fescue) antifreeze proteins and the polynucleotides
CC encoding them ADM41459-ADM41483. The polynucleotides were isolated from
CC tissues taken at different times of year (winter and spring) and from
CC different parts of the plants. The polynucleotides can be used to
CC modulate the cold tolerance of an organism, especially plants, mammals,
CC insects, fungi, archaea and bacteria. The method involves incorporating
CC an antifreeze polynucleotide, under the control of a gene promoter
CC sequence, into the genome of the organism, or introducing double-stranded
CC RNA corresponding to the polynucleotide into the cells of the organism,
CC thereby inhibiting expression of an antifreeze polypeptide. The
CC antifreeze protein can be used for the cryopreservation of a cell or
CC tissue, as a food additive of a frozen food product, in a method for
CC decreasing the time required to dehydrate a composition, to treat a
CC disorder characterised by biocrystals associated with disorders such as
CC gout and kidney stones, to preserve the viability of a molecular biology
CC reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
CC to protect a plant from damage due to frost or freezing.

	Best Local Similarity	70.3%; Pred.	No. 6e-120;
Matches	701; Conservative	0; Mismatches	206; Indels
Gaps	90;		
7;			
Qy	33	CATGCCTGAATACATGCAAGTGTTCACGTGCTGGTCTTTTGCGGTTCATTCTTGC	92
Dz	46	CCAGAACTTAATCATTGCGAAGAATGTTGGCTGCTGCTGCTCTTCTTGSTGTTCTCTTGC	105
Qy	93	AGTGGCAGGAGAACGTCGTGGTGTGCCACCACGACGACTCCAACGCGTTGAGGGGCC	152
Dz	106	TGGCCATGAGCGCAC-----GTCGTGCCACCTGGATGACTCCGCGCGCTGCGGGGCT	159
Qy	153	TCGCTGAGAACTTAAGCGCAAAGGAGCGCTCGCCTCCGCGCGCGCATGFTCCCGCGGCT	212
Dz	160	TTGTCGGGAACCTCAATGTC---GGGGGTGCCCTTCTCCGTGGAAATGGTCTGCTCCT	216
Qy	213	CATGCTGAGCTGGGAAGTGTGGGATGCGAAAACAGCAAGCGCGCGCTCGTGGCGTTGC	272
Dz	217	CATGCTGCAATGGAAGTGTGGCTGCGATGGTACAAGCGCGCGCTCACGCGGTTC	276
Qy	273	GGCTCC-----CCCCCCCCCC-----CCAAAGCGCG	287
Dz	277	GGCTTCGGATTAGCTCTGAGGACTGCGTAAGCTCAAGTCGCTCAACCTTCGCCAACAAAA	336
Qy	288	GCCTTGGAGGATCATCCATCGCTCGATTGTGTGAGCTTGATCACCCTTCGCTATTGGATC	347
Dz	337	GATTGGTTGGCACCATCCCCTCGTGGATTTGTGAGCTTGACAACAATTTGCTACTTGGTTC	396
Qy	348	TCTCGGCTAATTCATTGGTTGGGAGGTATCC-----AAAAAAAAAGTTTGCAGATAC	395
Dz	397	TCTCGGATAATTCATTGGTTGGTAAGGACCCCAATAGTTTTGCACNAATAGTTTGCAGATA	456
Qy	396	GGCTCAAGAGCCTCACCACTGACAGCCAGTCACTCGGTATGGTTCATTAACATGCTAT	455
Dz	457	GACTCAAGGGCTCGCCACCCTGCTGCTCACTAGGTATGGCTTTTCGCTAACATGCCAT	516
Qy	456	TGCATGTGA---GCAGTAGAAGACGCTCGATGAGAACCAAAATACATATACAGGACCA	512
Dz	517	TGCATGTGAAGGGAAACGAAGAACCCTTCGACGAAACAAACAAATACAAATCATGGAGCA	576
Qy	513	ACAATAGTGTGGATCAGGGAGCAACAATGTGTTTTCGCGGAATGACAAACCGTCTGAT	572
Dz	577	ACAACATGTTAGATCTGGGAACGACAATGCTGTTTTCGGGAACGACAACTGCTCAT	636
Qy	573	CTGGGAATAACAACATGTCCTGGAGCAACAACATGTTGTGTAATCTGGAAGTGAACAATA	632
Dz	637	GTGGGAACAAACAACCTGTGCTGGGAGCAACAACCATTTGCATCTGGCAGTGAACAATA	696
Qy	633	CTGTAGTTGTGTAGCAACCATGCTGATCAGGAGCAAAAGCATATTGTTACTGATAACAATA	692
Dz	697	TCGTAATCTGGCAGCAACCATATTGTATGTGGGACCAAAACATATCANAACTGATTAACA	756
Qy	693	ATGTTGTATCCGGAAACGACAATAATGTGTCTGGAAGCTTCCATCTGTATCAGGGAGC	752
Dz	757	ATGACGTATCCGGCAATGATAATAATGTTATCTGGGAGCTTCCATCTGTATCCGGAGCC	816
Qy	753	ACAATACGTATCCGGGAGCAACAATATCTGTATCTGGGAGCAACAATATCTGTATCTGGGA	812
Dz	817	ACAATACTGTATCTGGAGTAAACAACATGTATCTGGAAGCAACCATGCTGTATCTGGAA	876
Qy	813	GCAACAAGTCGTAAACAGATGTTAAATATCTGTAG-----TGCG--	852
Dz	877	GCAACAACCTGTGACGAGATGAATGATTTGTGAGGGGATTTGCTTCATCTTTCTCTAA	936
Qy	853	AGGATTTGCTTCATCTTCCCAAGTTTCAGTGTAGCTTACAATCAATFAGATGGAGACAATCA	912
Dz	937	AGGAGCTCTCACCCCTAGTCCAACTTCGCTGAGCTCAACAATCACTTTGTAGGGACAATCG	996
Qy	913	CGTTATGTAACTCA-GGATATGGCAATCTTTTCCTT	948
Dz	997	AGTTATGTAACTTCATGGATATAGCATCATTTCTCCCT	1033

RESULT 11

Query Match	40.2%	Score 394.4;	DB 12;	Length 1064;
Best Local Similarity	67.2%	Pred. No. 1e-112;		
Matches 711; Conservative	0;	Mismatches 226;	Indels 121;	Gaps 6;

ADW41465
ID ADW41465 standard; cDNA; 1064 BP.
XX
AC ADW41465;
XX
XX 03-JUN-2004 (first entry)
XX
XX Perennial ryegrass antifreeze protein AFP4 cDNA.
XX
XX Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;
KW antigout; litholytic; nephrotropic; cytostatic; gene; ss.
XX
XX Lolium perenne.
XX
XX Key Location/Qualifiers
XX CDS 55..897
XX FT /*tag= b
XX FT /product= "Antifreeze protein AFP4"
XX FT sig_peptide 55..120
XX FT /*tag= a
XX FT mat_peptide 121..894
XX FT /*tag= c
XX
XX W02004022700-A2.
XX
XX 18-MAR-2004.
XX
XX 09-SEP-2003; 2003WO-NZ000199.
XX
XX 09-SEP-2002; 2002US-0409557P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX (WRIG-) WRIGHTSON SEEDS LTD.
XX
XX Demmer J, Shenk WA, Hall C, Fish SA;
XX
XX WPI; 2004-248453/23.
XX P-PSDB; ADW41478.
XX
XX New antifreeze proteins and encoding polynucleotides, useful for
PT modulating cold tolerance in organisms, as food additives, or for
PT treating tumors or disorders associated with the presence of unwanted
PT biocrystals (e.g. gout).
XX
XX Claim 1; SEQ ID NO 8; 71pp; English.
XX
XX The present sequence is that of cDNA encoding AFP4, an antifreeze protein
CC of perennial ryegrass. The cDNA was isolated from a leaf and pseudostem
CC cDNA expression library. The invention provides forage grass (perennial
CC ryegrass and tall fescue) antifreeze proteins and the polynucleotides
CC encoding them ADW41458-ADW41483. The polynucleotides were isolated from
CC tissues taken at different times of year (winter and spring) and from
CC different parts of the plants. The polynucleotides can be used to
CC modulate the cold tolerance of an organism, especially plants, mammals,
CC insects, fungi, archaea and bacteria. The method involves incorporating
CC an antifreeze polynucleotide, under the control of a gene promoter
CC sequence, into the genome of the organism, or introducing double-stranded
CC RNA corresponding to the polynucleotide into the cells of the organism,
CC thereby inhibiting expression of an antifreeze polypeptide. The
CC antifreeze protein can be used for the cryopreservation of a cell or
CC tissue, as a food additive of a frozen food product, in a method for
CC decreasing the time required to dehydrate a composition, to treat a
CC disorder characterised by biocrystals associated with disorders such as
CC gout and kidney stones, to preserve the viability of a molecular biology
CC reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
CC to protect a plant from damage due to frost or freezing.
XX
XX Sequence 1064 BP; 263 A; 274 C; 267 G; 260 T; 0 U; 0 Other;


```
QY 383 AGTTTCAGATACGGCTCAAGACCTCACCACCTGACAGCGAGTCACTCGGTATGGGTCC 442
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
292 AGTTTCAGATATGCTCAAGAGGCTCACCACCGTGGCGGTCACTGGTAAAGGGTTC 351
QY 443 ATTAACATGCTATTGCTATGACGACAGTAG---NAGAACGCTGATGAAGAACCAATACA 499
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
352 ACTAACATGCCATTATCATGTGAAGTCTAGCCAAAGGAACACTGACGAAGAACCAATACA 411
QY 500 ATATCAGGAGACCAACAATAGTGTGGATCAGGAGGCAACAATGTTTCCGGGAATGAC 559
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
412 ATAACTGGGATCAACATATCTGCAATCCGGAGGCAACAATGTTTCTGGGAAGAT 471
QY 560 AACACCGTCTGATCTGGGAATAACAACCATGTTCTGGAGCAACAACACTGTTGTAAT 619
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
472 AACACTGTCTATCTCGGGAACAACAACGTCGTCTCGGGAGCCACAACAACCGTCTGATTT 531
QY 620 GGAAGTGACAACTACTAGTGTGTAGCAACCATGTCGTATCAGGGAACAAGCATATTGTT 679
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
532 GGGGGTGACAAATTTCTTAAGCGGTAGCAACCATGTCGTATCTGGGAACCAACCATGTCGTG 591
QY 680 ACTGATAACAATAATGTTGATCCGGGAACGACAATAATGTCGTGGAAGCTTCCATACT 739
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
592 ACTGACACAAGATGCGGTATCCGGGACCAACATATCTGTATCTGGAGCCAAATATACC 651
QY 740 GTATCAGGAGGACCAATATCCGTATCCGGGACCAACAATATCTGTATCCGGGAGCAACCAT 799
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
652 GTATCCGGGAACCAACCATATCATATCTGGAGCCACAGTACCATATCCGGGAACCAAT 711
QY 800 ATCGTATCTGGGAGGACCAAGTCGTAAACAGATGGTTAATATCTGTAGGTG 851
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
712 ACCGTATCCGGGAGCAACAATTTCTGTATCTGGGAACAACAATATTTGTATCTG 763
```

RESULT 13

```
AAX99717
ID AAX99717 standard; DNA; 357 BP.
XX
AC AAX99717;
XX
DT 29-SEP-1999 (first entry)
XX
DE Grass anti-freeze protein coding sequence.
XX
KW Anti-freeze protein; grass; plant; frozen food product; frost tolerance;
KW frozen confectionery; ss.
XX
OS Lolium perenne.
XX
PN WO9937782-A2.
XX
PD 29-JUL-1999.
XX
PF 23-DEC-1998; 98WO-EP008553.
XX
PR 22-JAN-1998; 98GB-00001408.
XX
PA (UNIL ) UNILEVER NV.
PA (UNIL ) UNILEVER PLC.
XX
PI Jarman CD, Sidebottom CM, Twigg S, Worrall D;
XX
DR WPI; 1999-458697/38.
DR P-PSDB; AAY22472.
XX
PT New plant anti-freeze protein useful in frozen food products.
XX
PS Claim 8; Page 37; 39pp; English.
XX
CC This sequence encodes the plant anti-freeze protein of the invention. The
CC anti-freeze protein is characterised in that at least 40% of its amino
CC acids are from the group of serine, threonine and asparagine. The anti-
CC freeze protein can be used in frozen food products, especially frozen
```

```
CC confectionery. Anti-freeze proteins are especially used in food products,
CC which are heated, e.g. by pasteurisation, blanching or sterilisation
CC prior to freezing. Plants transformed with a nucleic acid sequence
CC encoding the anti-freeze protein have an increased frost tolerance. Prior
CC art anti-freeze proteins have not been applied to commercially available
CC food products, due to high costs and complicated processes for obtaining
CC the protein. Also prior art anti-freeze proteins have tended to
CC destabilise during processing especially during the pasteurisation step.
CC This is overcome by the present anti-freeze protein. The anti-freeze
CC proteins provide an ice particle size following an ice recrystallisation
CC inhibition assay of 15 µm M or less. The anti-freeze protein ingredient
CC means that mixes can be frozen under quiescent conditions, e.g. in a shop
CC or home freezer without the formation of unacceptable ice crystal shapes
CC and hence with a texture different to products normally obtained via
CC quiescent freezing
XX
SQ Sequence 357 BP; 116 A; 80 C; 89 G; 72 T; 0 U; 0 Other;
```

```
Query Match 27.0%; Score 264.2; DB 2; Length 357;
Best Local Similarity 83.8%; Pred. No. 4.4e-72;
Matches 299; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
```

```
QY 482 GATGAAGAACCAATAACATATATCAGGAGCAACAATAGTGTGGATCAGGAGCAACAAT 541
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 GATGAACAGCCGAATACGATTTCTGGGAGCAACATACTGTCAATCCGGGAGCAAAAAT 60
QY 542 GTTGTTCCTCGGGAATGACAAACACCGTCTGTATCTGGGAATAACAACCATGTCTGGGAGC 601
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GTTCTTGTGGGATGACAAACACCGTCAATCTCTGGGAGCAACAATAGTGTCTGGGAGC 120
QY 602 AACACACTGTTGTAACTCGGAAGTGAACAATCTGTAGTGTGGTAGAACCATGTCTGATCA 661
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 AACACACTGTCGTAGTGGGAATGACAATACCGTAAACCGGAGCAACCATGTCTGATCA 180
QY 662 GGGACAAACCATATGTTACTGATACAAATAATGTTGTATCCGGGAGCAACAATATGTG 721
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 GGGACAAACCATATGTTACTGATACAAACAATAACGTATCCGGGAGCAACAATATATGTA 240
QY 722 TCTGGAAGCTTCCATCTGTATCAGGAGGAGCAACAATACCGTATCCGGGAGCAACAATCT 781
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 TCCGGAGGCTTTCATACCGTATCCGGGGGCGACATACTGTGTCCGGGAGCAACAATACC 300
QY 782 GTATCCGGGAGCAACAATATCGTATCTGGGAGCAACAAGTCTGTAAACAGATGTTAA 838
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 GTATCTGGGAGCAACCAACCGTGTGTCTGGAAGCAACAAGTCTGTACAGACGCTTAA 357
```

RESULT 14

```
ADM41458
ID ADM41458 standard; cDNA; 841 BP.
XX
AC ADM41458;
XX
DT 03-JUN-2004 (first entry)
XX
DE Perennial ryegrass antifreeze protein AFPl cDNA.
XX
KW Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant;
KW antigout; litholytic; nephrotropic; cytostatic; gene; ss.
XX
OS Lolium perenne.
XX
FH Key Location/Qualifiers
FT CDS 55..786
FT /tag= b
FT /product= "Antifreeze protein AFPl"
FT sig_peptide 55..114
FT /tag= a
FT mat_peptide 115..783
FT /tag= c
XX
PN WO2004022700-A2.
XX
```

PD 18-MAR-2004.
XX
XX
PF 09-SEP-2003; 2003WO-NZ000199.
XX
PR 09-SEP-2002; 2002US-0409557P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PA (WRIG-) WRIGHTSON SEEDS LTD.
XX
XX Demmer J, Shenk MA, Hall C, Fish SA;
XX
XX WPI; 2004-248453/23.
DR P-PSDB; ADM41471.
XX
XX
PT New antifreeze proteins and encoding polynucleotides, useful for
PT modulating cold tolerance in organisms, as food additives, or for
PT treating tumors or disorders associated with the presence of unwanted
PT biocrystals (e.g. gout).
XX
XX Claim 1; SEQ ID NO 1; 71pp; English.
XX
XX The present sequence is that of cDNA encoding APPI, an antifreeze protein
XX of perennial ryegrass. The cDNA was isolated from a pseudostem cDNA
XX expression library. The invention provides forage grass (perennial
XX ryegrass and tall fescue) antifreeze proteins and the polynucleotides
XX encoding them ADM41458-ADM41483. The polynucleotides were isolated from
XX tissues taken at different times of year (winter and spring) and from
XX different parts of the plants. The polynucleotides can be used to
XX modulate the cold tolerance of an organism, especially plants, mammals,
XX insects, fungi, archaea and bacteria. The method involves incorporating
XX an antifreeze polynucleotide, under the control of a gene promoter
XX sequence, into the genome of the organism, or introducing double-stranded
XX RNA corresponding to the polynucleotide into the cells of the organism,
XX thereby inhibiting expression of an antifreeze polypeptide. The
XX antifreeze protein can be used for the cryopreservation of a cell or
XX tissue, as a food additive of a frozen food product, in a method for
XX decreasing the time required to dehydrate a composition, to treat a
XX disorder characterised by biocrystals associated with disorders such as
XX gout and kidney stones, to preserve the viability of a molecular biology
XX reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
XX to protect a plant from damage due to frost or freezing.
XX
XX Sequence 841 BP; 216 A; 217 C; 222 G; 186 T; 0 U; 0 Other;
SQ

Query Match 26.8%; Score 262.2; DB 12; Length 841;
Best Local Similarity 73.5%; Pred. No. 3.1e-71;
Matches 349; Conservative 0; Mismatches 123; Indels 3; Gaps 1;
QY 380 AAAAGTTTGCAGATACGGCTCAAGAGCCTCACCACCTGACAGCCAGTCACTCGGTATGGGT 439
DB 262 AAGAGCTTCCAGATATTGCTCAAGGGCTCACCGCGCTGCGCTTCACTGGGTAAAGCG 321
QY 440 TCCATTACATGCTATTGTCATGTGAGCAGTAG---AAGAACGCTCGATGAAGAACCAAT 496
DB 322 TTCACTCACATGCCATTACATGTGAAGCCTAGCCAGGAACACCTCGAGGAAGACCAAT 381
QY 497 ACAATATCAGGAGCCACAATAGTGTGGATCAGGAGCACATGTGTTCCGGGAAT 556
DB 382 ACAATACTGGGATCAACAACTACTGTCTAGATCCGGGAGCAACAATGTTTCTGGGAAC 441
QY 557 GACACACGGTCTGTATCTGGGAATAACAACCATGTGTCTGGGAGCAACACATGTTGTA 616
DB 442 GATAACACTGTCAATATCCGGGAACACAACTGCTGTCTGGGAGCCACACCGTGTGA 501
QY 617 ACTGAAGTGAACATATCTGTAGTGTGGTAGCAACCATGTCTGATCAGGAGCAACATATT 676
DB 502 TTTGGGGTGAACAATTCATAAGTGAAGTGTACCATGTCTGATCTGGGAACCAACCATGTT 561
QY 677 GTTACTGATACATAATGTTGTATCCGGGAACGACATATATGTCTGGAAGCTTCCAT 736
DB 562 GTGACTGACAAAGAAATGCCGTATCCGGGAGCACAACTACTGTATCTGGHANGCAAAT 621
QY 737 ACTGTATCAGGGAGGACAAATACCGTATCCGGGAGCAACAATACTGTATCTGGGAGCAAC 796

DB 622 ACCGTATCCGGGAACCAACCAAGTATCTGGGAGCCACAGTACGTATCCGGGAACAC 681
QY 797 CATATCGTATCTGGGAGCAACAAAGTCTGAACAGATGGTTAAATTTCTGTAGGTG 851
DB 682 AATACGGTATCTGGGAGAAACAATTCGGTATATCGGAACAACAATATTGTATCTG 736
RESULT 15
ID ADJ40496
AC ADJ40496 standard; cDNA; 4536 BP.
XX
XX ADJ40496;
XX
DT 06-MAY-2004 (first entry)
DE DE
XX Plant cDNA #1496.
XX
KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
XX antifungal.
XX
OS Eukaryota.
XX
FN US2004016025-A1.
XX
PD 22-JAN-2004.
XX
XX 26-SEP-2002; 2002US-00260238.
XX
PR 26-SEP-2001; 2001US-0325277P.
PR 26-SEP-2001; 2001US-0325448P.
PR 04-APR-2002; 2002US-0370620P.
XX
XX (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KEEP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
XX
XX Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
XX Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
XX WPI; 2004-190374/18.
XX
XX New rice promoter, useful for manipulating crop plants to alter or
XX improve phenotypic characteristics e.g. produce large quantities of oil
XX or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX or high nutritional value.
XX
XX Claim 25; SEQ ID NO 1496; 230pp; English.
XX
XX The invention relates to plant nucleotide sequences that direct seed-,
XX leaf- and/or stem-, panicle-, root- or pollen-specific or preferential
XX or constitutive transcription of an operatively linked nucleic acid
XX segment. The invention also relates to a method for augmenting a plant
XX genome and a method of identifying a gene, where its expression is
XX altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
XX in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
XX canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
XX sorghum, rice or wheat. The polynucleotides and the polypeptides they
XX encode are useful for manipulating crop plants to alter or improve
XX phenotypic characteristics, to produce large quantities of oil or
XX proteins, to incur resistance to insecticides, viruses or fungi, and to

CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 4536 BP; 1102 A; 1247 C; 1221 G; 965 T; 0 U; 1 Other;

```
Query Match      8.1%; Score 79.4; DB 12; Length 4536;
Best Local Similarity 63.1%; Pred. No. 2.2e-13;
Matches 157; Conservative 0; Mismatches 86; Indels 6; Gaps 2;

QY 104 GCAACGTCGTGGTCCACACGACGACCTCCACGCGTTGAGGGGCGCTCGCTGAGAAC 163
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 76 GCTGGCGGCGCGCATGCCACCCGGAAGACCTCTCGCGCTGCGGGCATTTCGGGGGAAAT 135

QY 164 CT---AAGCGGCAAGAGAGCGTCCGCTCCGGCGCGCATGGTCCGGCGGCTCATGCTGC 220
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 136 CTCTCTGCGGGTGGGGCGCGCGCGGACTCCGGCGCGGTGGTCCGGGTGACGCGCTGCTGC 195

QY 221 AGCTTGGGAAGTGTGGGATCGGAACAGCAAGCGCGCGCTCGTGGGTTGCGGCTCCCC 280
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 196 GCCTGGGACGCGCTCGCTCGGACGCGC---CGCCGAGTCACGGCGCTGCGGCTCCCC 252

QY 281 AAGCGGCGCTTGGAGGGATCATCCCATCGTTCGATTGGTGAGCTTGATCACCTTTCGCTAT 340
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 253 GGGCGAGGTCTCGAGGGGGCCCATCCGCGCTCCCTCGCGGCGCTCGCGGCGCTCCAGGAC 312

QY 341 TTGGATCTC 349
    ||| ||| |||
Db 313 CTCGACCTC 321
```

Search completed: May 11, 2005, 00:27:35
Job time : 657 secs

Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 11, 2005, 01:34:03 ; Search time 704 Seconds
(without alignments)
8511.756 Million cell updates/sec

Title: US-10-657-852A-3
Perfect score: 980
Sequence: 1 gtttcattccaatcaagtg.....ccctttacataaaaaaaa 980

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 5654200 seqs, 3057283753 residues

Total number of hits satisfying chosen parameters: 11308400

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCIRUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79.4	8.1	3285	18 US-10-437-963-77805	Sequence 77805, A
2	79.4	8.1	4536	17 US-10-260-238-1496	Sequence 1496, Ap
3	50.8	5.2	2883	18 US-10-437-963-4582	Sequence 4582, Ap
4	50.6	5.2	1912	17 US-10-260-238-568	Sequence 568, App
5	50.6	5.2	2037	18 US-10-437-963-47843	Sequence 47843, A
C 6	45.4	4.6	2498	13 US-10-027-632-102064	Sequence 102064, A
C 7	45.4	4.6	2498	13 US-10-027-632-102065	Sequence 102065, A
C 8	45.4	4.6	2498	13 US-10-027-632-102066	Sequence 102066, A
C 9	45.4	4.6	2498	17 US-10-027-632-102064	Sequence 102064, A
C 10	45.4	4.6	2498	17 US-10-027-632-102065	Sequence 102065, A
C 11	45.4	4.6	2498	17 US-10-027-632-102066	Sequence 102066, A

C	12	44.8	4.6	1614	18 US-10-437-963-79739	Sequence 79739, A
	13	44.8	4.6	3453	14 US-10-101-464A-861	Sequence 861, App
	14	44.8	4.6	3453	19 US-10-864-252-861	Sequence 861, App
	15	44.6	4.6	2589	18 US-10-437-963-47358	Sequence 47358, A
	16	43.8	4.5	235070	13 US-10-087-192-1990	Sequence 1990, Ap
	17	43.4	4.4	485	18 US-10-425-115-155868	Sequence 155868, A
C	18	43.4	4.4	1504	18 US-10-719-993-27	Sequence 27, Appl
	19	43.4	4.4	1569	18 US-10-719-993-26	Sequence 26, Appl
C	20	43.4	4.4	37305	18 US-10-437-963-7515	Sequence 7515, Ap
	21	42.8	4.4	2379	18 US-10-437-963-7515	Sequence 7515, Ap
C	22	42.4	4.3	632	17 US-10-424-599-138064	Sequence 138064, A
	23	42.4	4.3	990	18 US-10-425-115-105088	Sequence 105088, A
	24	42.4	4.3	2485	17 US-10-425-114-24982	Sequence 24982, A
C	25	42.2	4.3	2268	18 US-10-437-963-39626	Sequence 39626, A
	26	42.2	4.3	2423	18 US-10-425-115-3469	Sequence 3469, Ap
C	27	41.8	4.3	492	18 US-10-767-701-22961	Sequence 22961, A
	28	41.8	4.3	3276	18 US-10-437-963-30048	Sequence 30048, A
C	29	41.4	4.2	966	18 US-10-363-345A-3863	Sequence 3863, Ap
	30	41.4	4.2	966	18 US-10-363-345A-3864	Sequence 3864, Ap
C	31	41.4	4.2	966	19 US-10-363-483A-3863	Sequence 3863, Ap
	32	41.4	4.2	966	19 US-10-363-483A-3864	Sequence 3864, Ap
	33	41.4	4.2	408	14 US-10-101-464A-212	Sequence 212, App
	34	41	4.2	408	19 US-10-864-252-212	Sequence 212, App
	35	41	4.2	667	18 US-10-425-115-67222	Sequence 67222, A
C	36	40.8	4.2	3111	18 US-10-437-963-47196	Sequence 47196, A
	37	40.8	4.2	3696	18 US-10-437-963-430	Sequence 430, App
C	38	40.4	4.1	333	18 US-10-437-963-98336	Sequence 98336, A
	39	40.4	4.1	396	14 US-10-101-464A-221	Sequence 221, App
	40	40.4	4.1	396	19 US-10-864-252-221	Sequence 221, App
	41	40.4	4.1	3381	10 US-09-952-267-6	Sequence 6, Appl
C	42	40.4	4.1	12614	17 US-10-242-355-1086	Sequence 1086, Ap
	43	40.2	4.1	1048	17 US-10-424-599-95215	Sequence 95215, A
	44	39.8	4.1	3330	18 US-10-437-963-64573	Sequence 64573, A
	45	39.6	4.0	1671	18 US-10-437-963-7514	Sequence 7514, Ap

ALIGNMENTS

RESULT 1
US-10-437-963-77805
; Sequence 77805, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 77805
; LENGTH: 3285
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(3285)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_7766C.1
US-10-437-963-77805

Query Match 8.1%; Score 79.4; DB 18; Length 3285;
Best Local Similarity 63.1%; Pred. No. 2.2e-14;
Matches 157; Conservative 0; Mismatches 86; Indels 6; Gaps 2;

QY 104 GCAAGTCGTGTCGTGCACCAACGACGACCTCCACGGGTTGAGGGGCTCGCTGAGAAC 163
Db 76 GCTGGGGGGCCATGACCCGGAAGACCTTCCTCGCGCTGCGGGGATTTGCGGGGAAT 135
QY 164 CT---AAGCGGCAAGAGCCGTCCGCTCCGCGCGCATGTCGCGGCGCTCATGCTGC 220
Db 136 CTCTCTGCGGGTGGGGGGCGCGGACTCCGCGCGCGGTGGTGGGTGACGCGCTGCTGC 195
QY 221 AGCTGGGAAGTGTGGGATGCGAAACAGACAGCGCGCGCTGCTGCGGCTTGGCGGCTCCCC 280
Db 196 GCCTGGGACGGCGTCCCTGCGACGCCG---CGCCGAGTACAGCGCGCTGCGGCTCCCC 252
QY 281 AAGCGCGCTTGGAGGATCATCCATCGATTGCTGAGCTTGATCATCTTGGCTAT 340
Db 253 GGGCGAGTCTCGAGGGGCCCATCCCGCTCCCTCGCGCGCTCGCGGCTCCAGGAC 312
QY 341 TTGGATCTC 349
Db 313 CTCGACCTC 321

RESULT 2

US-10-260-238-1496
; Sequence 1496, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 1496
; LENGTH: 4536
; TYPE: DNA
; ORGANISM: Oryza sativa
; NAME/KEY: N region
; LOCATION: (661)..(661)
; OTHER INFORMATION: n = any nucleotide
US-10-260-238-1496

Query Match 8.1%; Score 79.4; DB 17; Length 4536;
Best Local Similarity 63.1%; Pred. No. 2.7e-14;
Matches 157; Conservative 0; Mismatches 86; Indels 6; Gaps 2;
QY 104 GCAAGTCGTGTCGTGCACCAACGACGACCTCCACGGGTTGAGGGGCTCGCTGAGAAC 163
Db 76 GCTGGGGGGCCATGACCCGGAAGACCTTCCTCGCGCTGCGGGGATTTGCGGGGAAT 135
QY 164 CT---AAGCGGCAAGAGCCGTCCGCTCCGCGCGCATGTCGCGGCGCTCATGCTGC 220
Db 136 CTCTCTGCGGGTGGGGGGCGCGGACTCCGCGCGCGGTGGTGGGTGACGCGCTGCTGC 195
QY 221 AGCTGGGAAGTGTGGGATGCGAAACAGACAGCGCGCGCTGCTGCGGCTTGGCGGCTCCCC 280

Db 196 GCCTGGGACGGCTCGCTCGACGCCG---CGCCGAGTACAGGGGCTCGGCTCCCC 252
QY 281 AAGCGCGCTTGGAGGATCATCCATCGATTGCTGAGTGTGATCATCTTGGCTAT 340
Db 253 GGGCGAGTCTCGAGGGGCCCATCCCGCTCCCTCGCGCGCTCGCGGCTCCAGGAC 312
QY 341 TTGGATCTC 349
Db 313 CTCGACCTC 321

RESULT 3

US-10-437-963-4582
; Sequence 4582, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 4582
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_11452C.1
US-10-437-963-4582

Query Match 5.2%; Score 50.8; DB 18; Length 2883;
Best Local Similarity 56.6%; Pred. No. 5.5e-05;
Matches 94; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 117 CGTGCCACACGACGACCTCCACGGCTTGGAGGGGCTCGCTGAGAACCTAAGCGGCAAG 176
Db 104 CTGCGTCCCGAGGAGCGGGCGGCTTCGCGCATCAAGCTGGCTTACAGCGACC 163
QY 177 GAGCGCTCCGCTCCGCGCGCATGTCCGCGCGCTCATGCTGAGCTGGGAAGGTGG 236
Db 164 CGAGCGCGCTCGCTGCTGGGGCGCGCGGCGGCTGCTGCGGTGGAGCGGCTCG 223
QY 237 GATCGAAACAGGAGCGGCGGCTGCTGGGCTTGGCGCTCCCCAA 282
Db 224 TCTCGACAACGCCGCCACGCTACGAGGCTGAGGCTCCCAA 269

RESULT 4

US-10-260-238-568
; Sequence 568, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP

; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 568
; LENGTH: 1912
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-568

Query Match 5.2%; Score 50.6; DB 17; Length 1912;
Best Local Similarity 48.1%; Pred. No. 5e-05;
Matches 143; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 84 TCATCTTGAGGTGGCAGGAGCAACGTCGTGGTGGTCCACACGAGACCTCCAGCGGT 143
DB 32 TCCTCTCTCTCGCGGTCTTTCGCGCGCCTCATCGCGCAACGAGAGGCGCGCGC 91
QY 144 TGAGGGSCCTCGCTGAGAACCTAAGCGCAAGAGCGCTCCGCTCCGCGCCGATGTT 203
DB 92 TGATGGCGCTCAAGAGAGCGCTTGACCCGCGCGGCGGTGCTGGGCTCGTGGGCGCGT 151
QY 204 CCGCGCGCTCATGCTGAGCTGGGAGGTGTGGGATGCGAAACAGACGAGCGCGCGTGC 263
DB 152 CCGCGAGCGCTTGGCGGGGCTGTTTCGTCGGCGTGCAGCGAGCGCGCGGTGA 211
QY 264 TGGCGTTGGCGTCCCAAGCGCGGCTTGGAGGGATCATCCCATCGTCCGATTTGGTGC 323
DB 212 CGGCCATCTCGCTGACGAGCGCGGCTCTCCGGAGCCCTCTCCGCGGCGTATACCCA 328

RESULT 5
US-10-437-963-47843
; Sequence 47843, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 47843
; LENGTH: 2037
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_50573C.1
US-10-437-963-47843

Query Match 5.2%; Score 50.6; DB 18; Length 2037;
Best Local Similarity 48.1%; Pred. No. 5.2e-05;
Matches 143; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 84 TCATCTTGAGGTGGCAGGAGCAACGTCGTGGTGGTCCACACGAGACCTCCAGCGGT 143

DB 32 TCCTCTCTCTCGCGGTCTTTCGCGCGCCTCATCGCGCAACGAGAGGCGCGCGCGC 91
QY 144 TGAGGGSCCTCGCTGAGAACCTAAGCGCAAGAGCGCTCCGCTCCGCGCCGATGTT 203
DB 92 TGATGGCGCTCAAGAGAGCGCTTGACCCGCGCGGCGGTGCTGGGCTCGTGGGCGCGT 151
QY 204 CCGCGCGCTCATGCTGAGCTGGGAGGTGTGGGATGCGAAACAGACGAGCGCGCGTGC 263
DB 152 CCGCGAGCGCTTGGCGGGGCTGTTTCGTCGGCGTGCAGCGAGCGCGCGGTGA 211
QY 264 TGGCGTTGGCGTCCCAAGCGCGGCTTGGAGGGATCATCCCATCGTCCGATTTGGTGC 323
DB 212 CGGCCATCTCGCTGACGAGCGCGGCTCTCCGGAGCCCTCTCCGCGGCGTATACCCA 328

RESULT 6
US-10-027-632-102064/c
; Sequence 102064, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102064
; LENGTH: 2498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-102064

Query Match 4.6%; Score 45.4; DB 13; Length 2498;
Best Local Similarity 51.9%; Pred. No. 0.003;
Matches 123; Conservative 1; Mismatches 112; Indels 1; Gaps 1;

QY 600 GCAACAACTGTTGTAAGTGAACAATACTAGTGTGGTAGCAACCATGTCTAT 659
DB 346 GAAGCATCCAGTGGAAACAGGAGCATGCAGATGGAACAGAAATGTCAGCATGGA 287
QY 660 CAGGGA-CAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAAT 718
DB 286 CAGGAAGCAATCCAGAAATGGAACAGGGAGCATCCAGATGGAACAGAAATGTCAGCAT 227
QY 719 GTGTCCTGGAAGTTCCTACTGATATCAGGGGAGCAATACCTATCCGGAGCAACAT 778
DB 226 GGAACAGGAGCATCCAGCATGGAACAGGAGCGTCAAGCGTGAACAGGAGCGTCAAG 167
QY 779 ACTGTATCCGGAGCAACCATATCGTATCTGGAGCAACAAGTCCGTAAACAGATGTT 835
DB 166 CGTGGAAAGGAGCGTCAAGCGTGAACAGGAGCGTCCAGCGTGAACAGGAGT 110

```
RESULT 7
US-10-027-632-102065/c
; Sequence 102065, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102065
; LENGTH: 2498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-102065

Query Match          4.6%; Score 45.4; DB 13; Length 2498;
Best Local Similarity 51.9%; Pred. No. 0.003;
Matches 123; Conservative 1; Mismatches 112; Indels 1; Gaps 1;

QY 600 GCAACAACACTGTTGTAACCTGGAAGTGCACATACTGTAGTTGGTAGCAACCATGTCGTAT 659
Db 346 GAAGCATCCAGATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 287
QY 660 CAGGGA-CAAGCATATTGTTACTGATACCAATATGTTGTTATCCGGGAGCAACAAT 718
Db 286 CAGGAAGCAATCCAGAAATGGAACAGGAGCATCCAGAGTGGAAACAGGAATGTCAGCAT 227
QY 719 GTGTCGGAAGCTTCCATCTGATCTGAGGAGGAGCAATACCGTATCCGGGAGCAACAAT 778
Db 226 GGAACAGGAGAGCATCCAGCATGGAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 167
QY 779 ACTGTATCCGGGAGAGCAACCATATCTGTATCTGGGAGCAACAAGTCGTAACAGATGGT 835
Db 166 CGTGGACAGGAGAGCGTCMAGCGTGGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGT 110

RESULT 8
US-10-027-632-102066/c
; Sequence 102066, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102066
; LENGTH: 2498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-102066

Query Match          4.6%; Score 45.4; DB 13; Length 2498;
Best Local Similarity 51.9%; Pred. No. 0.003;
Matches 123; Conservative 1; Mismatches 112; Indels 1; Gaps 1;

QY 600 GCAACAACACTGTTGTAACCTGGAAGTGCACATACTGTAGTTGGTAGCAACCATGTCGTAT 659
Db 346 GAAGCATCCAGATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 287
QY 660 CAGGGA-CAAGCATATTGTTACTGATACCAATATGTTGTTATCCGGGAGCAACAAT 718
Db 286 CAGGAAGCAATCCAGAAATGGAACAGGAGCATCCAGAGTGGAAACAGGAATGTCAGCAT 227
QY 719 GTGTCGGAAGCTTCCATCTGATCTGAGGAGGAGCAATACCGTATCCGGGAGCAACAAT 778
Db 226 GGAACAGGAGAGCATCCAGCATGGAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 167
QY 779 ACTGTATCCGGGAGAGCAACCATATCTGTATCTGGGAGCAACAAGTCGTAACAGATGGT 835
Db 166 CGTGGACAGGAGAGCGTCMAGCGTGGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGT 110
```

```
US-10-027-632-102066/c
; Sequence 102066, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102066
; LENGTH: 2498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-102066

Query Match          4.6%; Score 45.4; DB 13; Length 2498;
Best Local Similarity 51.9%; Pred. No. 0.003;
Matches 123; Conservative 1; Mismatches 112; Indels 1; Gaps 1;

QY 600 GCAACAACACTGTTGTAACCTGGAAGTGCACATACTGTAGTTGGTAGCAACCATGTCGTAT 659
Db 346 GAAGCATCCAGATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 287
QY 660 CAGGGA-CAAGCATATTGTTACTGATACCAATATGTTGTTATCCGGGAGCAACAAT 718
Db 286 CAGGAAGCAATCCAGAAATGGAACAGGAGCATCCAGAGTGGAAACAGGAATGTCAGCAT 227
QY 719 GTGTCGGAAGCTTCCATCTGATCTGAGGAGGAGCAATACCGTATCCGGGAGCAACAAT 778
Db 226 GGAACAGGAGAGCATCCAGCATGGAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 167
QY 779 ACTGTATCCGGGAGAGCAACCATATCTGTATCTGGGAGCAACAAGTCGTAACAGATGGT 835
Db 166 CGTGGACAGGAGAGCGTCMAGCGTGGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGT 110

RESULT 9
US-10-027-632-102064/c
; Sequence 102064, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102064
; LENGTH: 2498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-102064

Query Match          4.6%; Score 45.4; DB 17; Length 2498;
Best Local Similarity 51.9%; Pred. No. 0.003;
Matches 123; Conservative 1; Mismatches 112; Indels 1; Gaps 1;

QY 600 GCAACAACACTGTTGTAACCTGGAAGTGCACATACTGTAGTTGGTAGCAACCATGTCGTAT 659
```

Db 346 GAAGCATCCAGATGGGAACAGGAAGCATGCAGATGGAAACAGGAATGTCAGCATGGAA 287
QY 660 CAGGGA-CAAAGCATATTTACTGATAACAATAATTTCTATCCGGGAACGACAATAAT 718
Db 286 CAGGAAGCATCCAGATGGAAACAGGAGCATCCAGATGGAAACAGGAATGTCAGCAT 227
QY 719 GTGTCGGAAGCTTCCATATCTGTATCAGGGGAGCAAAATACCGTATCCGGGAGCAAAAT 778
Db 226 GGAACAGGAAGCATCCAGCATGGAAACAGGAAGCGTCAAGCGTGGAAACAGGAAGCGTCAAG 167
QY 779 ACTGTATCCGGGAGCAACCATATCTGTATCTGGAGCAACAAATCTGTACAGATGTT 835
Db 166 CGTGGAAACAGGAAGCGTCMAGCGTGGAAACAGGAAGCGTCCAGCGTGGAAACAGGAAGT 110

RESULT 10
US-10-027-632-102065/c
; Sequence 102065, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102065
; LENGTH: 2498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-102065

Query Match 4.6%; Score 45.4; DB 17; Length 2498;
Best Local Similarity 51.9%; Pred. No. 0.003;
Matches 123; Conservative 1; Mismatches 112; Indels 1; Gaps 1;
QY 600 GCAACAACTGTTGTAACAGGAGTGAACAATAATTTCTATCCGGGAGCAACCATATGTCGTAT 659
Db 346 GAAGCATCCAGATGGGAACAGGAAGCATGCAGATGGAAACAGGAATGTCAGCATGGAA 287
QY 660 CAGGGA-CAAAGCATATTTACTGATAACAATAATTTCTATCCGGGAGCAACCATAT 718
Db 286 CAGGAAGCATCCAGATGGAAACAGGAGCATCCAGATGGAAACAGGAATGTCAGCAT 227
QY 719 GTGTCGGAAGCTTCCATATCTGTATCAGGGGAGCAAAATACCGTATCCGGGAGCAAAAT 778
Db 226 GGAACAGGAAGCATCCAGCATGGAAACAGGAAGCGTCAAGCGTGGAAACAGGAAGT 167
QY 779 ACTGTATCCGGGAGCAACCATATCTGTATCTGGAGCAACAAATCTGTACAGATGTT 835
Db 166 CGTGGAAACAGGAAGCGTCMAGCGTGGAAACAGGAAGCGTCCAGCGTGGAAACAGGAAGT 110

RESULT 11
US-10-027-632-102066/c
; Sequence 102066, Application US/10027632

Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102066
; LENGTH: 2498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-102066
Query Match 4.6%; Score 45.4; DB 17; Length 2498;
Best Local Similarity 51.9%; Pred. No. 0.003;
Matches 123; Conservative 1; Mismatches 112; Indels 1; Gaps 1;
QY 600 GCAACAACTGTTGTAACAGGAGTGAACAATAATTTCTATCCGGGAGCAACCATATGTCGTAT 659
Db 346 GAAGCATCCAGATGGGAACAGGAAGCATGCAGATGGAAACAGGAATGTCAGCATGGAA 287
QY 660 CAGGGA-CAAAGCATATTTACTGATAACAATAATTTCTATCCGGGAGCAACCATAT 718
Db 286 CAGGAAGCATCCAGATGGAAACAGGAGCATCCAGATGGAAACAGGAATGTCAGCAT 227
QY 719 GTGTCGGAAGCTTCCATATCTGTATCAGGGGAGCAAAATACCGTATCCGGGAGCAAAAT 778
Db 226 GGAACAGGAAGCATCCAGCATGGAAACAGGAAGCGTCAAGCGTGGAAACAGGAAGT 167
QY 779 ACTGTATCCGGGAGCAACCATATCTGTATCTGGAGCAACAAATCTGTACAGATGTT 835
Db 166 CGTGGAAACAGGAAGCGTCMAGCGTGGAAACAGGAAGCGTCCAGCGTGGAAACAGGAAGT 110

RESULT 12
US-10-437-963-79739/c
; Sequence 79739, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 79739
; LENGTH: 1614
; TYPE: DNA

```

; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_7942C.1
US-10-437-963-79739

Query Match      4.6%; Score 44.8; DB 18; Length 1614;
Best Local Similarity 55.0%; Pred. No. 0.0036;
Matches 88; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 107 AGCTGTGTGCTGTCACACAGACACCTCCACGGCTTGAGGGGCTCGCTGAGAACCTA 166
Db 371 AGCCCGCTTTGACCCGACCGCCGACGCGGAGCGGAGCGGAGCGGAGCTC 312
QY 167 ACGGCGAAGAGCGCTCGCTCCGCGCCGATGTCGGGCGCTCATGCTGCGAGCTGG 226
Db 311 CGCCCGGGCTCTCGCTGTCGCCCGCGCGATGTCGGCGCGCTGACACGAGCGC 252
QY 227 GAAGGTGTGGATGCGAAACAGCAAGCGCGCGCTCGTGG 266
Db 251 GCGCGGAGGCGCGCTTGCGGAGGAGGAGCTTTGG 212

RESULT 13
US-10-101-464A-861
; Sequence 861, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 861
; LENGTH: 3453
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-101-464A-861

Query Match      4.6%; Score 44.8; DB 14; Length 3453;
Best Local Similarity 48.4%; Pred. No. 0.0059;
Matches 124; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 51 CAAAGTGTGATGCTGCTGCTCTTTGCGGTTCATCTTCAGGTGGCAGGACCAAGT 110
Db 3 CAATGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCGC 62
QY 111 CGTGTGCTGTCACACAGACACCTCCACGCGCTTGAGGGGCTCGCTGAGAACCTAAGCG 170
Db 63 CGGCGCTGTCCCTCAACAGGAGGCTCTACCTCCACGCGGCAAGCTCTCCCTCTCCG 122
QY 171 GCAAAGGAGCGCTCGGCTCCGCGCGCATGTCGGGCGCTCATGCTGAGCTGGGAAG 230
Db 123 ACCAGGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCGCG 182
QY 231 GTGTGGATGCGAAGACAGCAAGCGCGCTCGTGGGTTCGCGGTTCGCGGTTCGCGGCGGCC 290
Db 183 GCGTGGGTGCGAGCGGCGCTCTCCGCGCTCGCTCTCTCTCTCTCTCTCTCTCTCTCC 242
QY 291 TTGGAGGATCATCCC 306
Db 243 TCGGCGGCGCTTCCC 258

RESULT 15
US-10-437-963-47358
; Sequence 47358, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

```

```

Db 243 TCGGCGGCGCTTCCC 258

RESULT 14
US-10-864-252-861
; Sequence 861, Application US/10864252
; Publication No. US20050050583A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c3
; CURRENT APPLICATION NUMBER: US/10/864,252
; CURRENT FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: 10/101,464
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 861
; LENGTH: 3453
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-864-252-861

Query Match      4.6%; Score 44.8; DB 19; Length 3453;
Best Local Similarity 48.4%; Pred. No. 0.0059;
Matches 124; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 51 CAAAGTGTGATGCTGCTGCTCTTTGCGGTTCATCTTCAGGTGGCAGGACCAAGT 110
Db 3 CAATGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCGC 62
QY 111 CGTGTGCTGTCACACAGACACCTCCACGCGCTTGAGGGGCTCGCTGAGAACCTAAGCG 170
Db 63 CGGCGCTGTCCCTCAACAGGAGGCTCTACCTCCACGCGGCAAGCTCTCCCTCTCCG 122
QY 171 GCAAAGGAGCGCTCGGCTCCGCGCGCATGTCGGGCGCTCATGCTGAGCTGGGAAG 230
Db 123 ACCAGGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCGCG 182
QY 231 GTGTGGATGCGAAGACAGCAAGCGCGCTCGTGGGTTCGCGGTTCGCGGTTCGCGGCGGCC 290
Db 183 GCGTGGGTGCGAGCGGCGCTCTCCGCGCTCGCTCTCTCTCTCTCTCTCTCTCTCTCC 242
QY 291 TTGGAGGATCATCCC 306
Db 243 TCGGCGGCGCTTCCC 258

RESULT 15
US-10-437-963-47358
; Sequence 47358, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

```

Search completed: May 11, 2005, 04:32:56
Job time : 773 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2005, 23:56:18 ; Search time 4632 Seconds
(without alignments)
10251.751 Million cell updates/sec

Title: US-10-657-852A-3
Perfect score: 980
Sequence: 1 gttgtcattcccaatcaagt.....ccctttacataaaaaaaa 980

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	264.2	27.0	357	6	BD139942
2	264.2	27.0	357	6	AX019971 Sequence
3	264.2	27.0	357	8	LPE277399 Lolium pe
4	79.4	8.1	3392	8	AK121984 Oryza sat
5	79.4	8.1	149371	8	AP004342 Oryza sat
6	76	7.8	349418	3	CR382398 Plasmodiu
7	74.8	7.6	2238	8	AK064359 Oryza sat
8	74.8	7.6	2958	8	AK103166 Oryza sat
9	70.2	7.2	176237	9	CNS08CBF Human chr
10	67.2	6.9	169802	9	CNS01DT2 Human chr
11	63.8	6.5	646	8	AF372178 Leptocory
12	63.8	6.5	347582	3	PFMAL4P1 Plasmodiu
13	62.8	6.4	300	6	CQ741677 Sequence
14	60.8	6.2	261587	2	AC126139 Rattus no
15	59.6	6.1	172927	2	AC119701 Rattus no
16	58.2	5.9	290724	2	AC098103 Rattus no
17	57.8	5.9	231341	5	BX004816 Zebrafish
18	55.8	5.7	243639	2	AC109943 Rattus no
19	55.2	5.6	342650	1	AP003582 Nostoc sp

20	55	5.6	349418	3	CR382398	CR382398 Plasmodiu
21	54.2	5.5	243174	2	AC107550	AC107550 Rattus no
22	54.2	5.5	255300	2	AC128061	AC128061 Rattus no
23	54	5.5	2000	6	AX655393	AX655393 Sequence
24	54	5.5	167601	10	AC144408	AC144408 Mus muscu
25	54	5.5	217131	10	AC126053	AC126053 Mus muscu
26	53.6	5.5	56310	2	AC084717	AC084717 Homo sapi
27	53.6	5.5	222930	2	AC099698	AC099698 Mus muscu
28	53.6	5.5	289405	2	AC090126	AC090126 Mus muscu
29	53.2	5.4	110000	1	CR522870	CR522870 Desulfota
30	53.2	5.4	158901	2	AC145786	AC145786 xenopus t
31	52.6	5.4	41951	2	AC139177	AC139177 Clona sav
32	52.4	5.3	10029	1	AE010994	AE010994 Mechanosa
33	52.2	5.3	109137	2	AC116969	AC116969 Rattus no
34	52.2	5.3	172750	2	AC119495	AC119495 Rattus no
35	52.2	5.3	217434	2	AC133239	AC133239 Rattus no
36	52.2	5.3	236346	2	AC095765	AC095765 Rattus no
37	52	5.3	5940	8	THA13651	THA13651 Trichoder
38	51.8	5.3	1138	6	EO2599	EO2599 DNA encodin
39	51.8	5.3	4215	9	HSSIGMG4	X12843 Human sigma
40	51.8	5.3	200267	10	AL03606	AL03606 Mus muscu
41	51.6	5.3	193223	10	AL672010	AL672010 Mouse DNA
42	51.6	5.3	347582	3	PFMAL4P1	AL034557 Plasmodiu
43	51	5.2	190316	10	AC122470	AC122470 Mus muscu
44	51	5.2	192387	10	AC151578	AC151578 Mus muscu
45	50.8	5.2	97900	3	AC087422	AC087422 Caenorhab

ALIGNMENTS

RESULT 1	BD139942	357 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD139942				
DEFINITION	Frozen foods.				
ACCESSION	BD139942				
VERSION	BD139942.1 GI:23234887				
KEYWORDS	JP 2002504316-A/1.				
SOURCE	Lolium perenne				
ORGANISM	Lolium perenne				
REFERENCE	1 (bases 1 to 357)				
AUTHORS	Jarman,C.D., Sidebottom,C.M., Twigg,S. and Worrall,D.				
TITLE	Frozen foods				
JOURNAL	Patent: JP 2002504316-A 1 12-FEB-2002;				
COMMENT	UNILEVER NV				
	OS Lolium perenne (perennial ryegrass)				
	PN JP 2002504316-A/1				
	PD 12-FEB-2002				
	PF 23-DEC-1998 JP 2000528689				
	PR 22-JAN-1998 GB 9801408.7				
	PI CARL DUDLEY JARMAN, CHRISTOPHER MICHAEL SIDEBOTTOM, SARAH TWIGG,				
	PI DAWN WORRALL				
	PC C12N15/09,A01H5/00,A23G9/02,A23L3/375,C07K14/415,C12N15/00 CC				
	Frozen foods				
FT	Key	Location/Qualifiers			
FT	source	1..357			
	/organism='Lolium perenne (perennial ryegrass)'				
FEATURES	Location/Qualifiers				
source	1..357				
	/organism="Lolium perenne"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:4522"				
ORIGIN					
Query Match	27.0%;	Score 264.2;	DB 6;	Length 357;	
Best Local Similarity	83.8%;	Pred. No. 2.4e-60;			
Matches 299;	Conservative 0;	Mismatches 58;	Indels 0;	Gaps 0;	
QY	482	GATGAAGAACCAATACATATATCAGGGACCAACAATAGTGTGGATCAGGAGCAACAAT	541		

```

||||| 1 GATGAACGCCGAATACGATTCTTGGAGCAACATATGTCAGATCGGGAGCAAAAT 60
||||| 542 GTTGTTCGGGAATGACAAACGGTGTGATCTGGGAATAACCAACCATGTGTCTGGAGC 601
||||| 61 GTTCTTGTCTGGGAATGACAAACCGTCTATATCTGGGGACAAACAATAGTGTCTGGAGC 120
||||| 602 AACACACTGTGTAACCTGGAAGTACAAATCTAGTGTAGTGGTGGTGGTGGTATCA 661
||||| 121 AACACACTGTGTAAGTGGGAATGACAAATACCGTAACCGGAGCAACCAATGTGTGATCA 180
||||| 662 GGGCAAAAGCATATTTGTTACTGATAACAAATATGTTGATCTCGGGAACGCAATAATGTG 721
||||| 181 GGGCAAAACCATATGTTTACAGACAAACAATACGATCTCGGGAACGATAAATGTA 240
||||| 722 TCTGGAAGTCTTCATCTGTAACGAGGAGACAAATACCGTATCTCGGAGCAACAATACT 781
||||| 241 TCCGGAGCTTTTCATACCGTATCTCGGGGGGACAAATCTGTCTCGGAGCAACAATACC 300
||||| 782 GTATCCGGGAGCAACCATATGTTCTCGGAGCAACAAAGTCGTAACAGATGTTAA 838
||||| 301 GTATCTGGAGCAACCATGTTGTATCTGGAAGCAACAAAGTCGTGACAGACGCTTAA 357

```

```

RESULT 2
AX019971
LOCUS AX019971 357 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 2 from Patent WO9337782.
ACCESSION AX019971
VERSION AX019971.1 GI:10043803
KEYWORDS
SOURCE
ORGANISM

```

```

REFERENCE
AUTHORS Twigg, S., Worrall, D., Jarman, C. D. and Sidebottom, C. M.
TITLE Frozen food product
JOURNAL Patent: WO 9337782-A 2 29-JUL-1999;
TWIGG SARAH (GB); UNILEVER PLC (GB); WORRALL DAWN (GB); JARMAN CARL
DUDLEY (GB); SIDEBOTTOM CHRISTOPHER MICHAEL (GB); UNILEVER NV (NL)
LOCATION/Qualifiers

```

```

FEATURES
source
1..357
/organism="Lolium perenne"
/mol_type="unassigned DNA"
/db_xref="taxon:4522"

```

ORIGIN

```

Query Match 27.0%; Score 264.2; DB 6; Length 357;
Best Local Similarity 83.8%; Pred. No. 2.4e-60;
Matches 299; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 482 GATGAAGAACCAATACAAATATCAGGACCAACAAATAGTGTGGATCAGGAGCAACAAT 541
DB 1 GATGAACAGCGGAATACGATTCTCGGAGCAACAATATCTGTGATCGGAGCAAAAAT 60
QY 542 GTTGTTCGGGAATGACAAACCGTCTGATCTGGGATACCAACCATGTGTCTGGAGC 601
DB 61 GTTCTTGTCTGGGAATGACAAACCGTCTATCTCGGGACAAACAATAGTGTCTGGAGC 120
QY 602 AACACACTGTGTAACCTGGAAGTGAACAATCTGTAGTGTGTAACCAACCATGTGTGATCA 661
DB 121 AACACACTGTGTAAGTGGGAATGACAAATACCGTACCGGAGCAACCATGTGTGATCA 180
QY 662 GGGCAAAAGCATATTTGTTACTGATAACAATATGTTGATCTCGGGAACGCAATAATGTG 721
DB 181 GGGCAAAACCATATCGTTTACAGACAAACAATAACGATCTCGGGAACGATAAATGTA 240
QY 722 TCTGGAAGTCTTCATCTGTAACGAGGAGACAAATACCGTATCTCGGAGCAACAATACT 781
DB 241 TCCGGAGCTTTTCATACCGTATCTCGGGGGGACAAATCTGTGTCTCGGAGCAACAATACC 300

```

```

QY 782 GTATCCGGGAGCAACCATATGTTCTCGGAGCAACAAAGTCGTAACAGATGTTAA 838
DB 301 GTATCTGGAGCAACCATGTTGTATCTGGAAGCAACAAAGTCGTGACAGACGCTTAA 357

RESULT 3
LPE277399
LOCUS LPE277399 357 bp mRNA linear PLN 29-APR-2000
DEFINITION Lolium perenne partial mRNA for ice recrystallisation inhibition protein.
ACCESSION AJ277399
VERSION AJ277399.1 GI:7573547
KEYWORDS ice recrystallisation inhibition protein.
SOURCE Lolium perenne
ORGANISM

```

```

REFERENCE
AUTHORS Sidebottom, C. M.
JOURNAL Thesis (1999) University of York
REFERENCE 2 (bases 1 to 357)
AUTHORS Sidebottom, C. M.
TITLE Direct Submission
JOURNAL Submitted (11-APR-2000) Sidebottom C. M., Plant Science, Unilever Research, Colworth House, Sharnbrook, Bedfordshire, MK44 1LQ, UNITED KINGDOM
COMMENT cds represents presumed mature peptide generated by cleavage before the first amino acid.
FEATURES
source
1..357
Location/Qualifiers
/organism="Lolium perenne"
/mol_type="mRNA"
/db_xref="taxon:4522"
<1..357
/function="freezing tolerance"
/notes="ORF1"
/codon_start=1
/product="ice recrystallisation inhibition protein"
/protein_id="CA887814.1"
/db_xref="GI:7573548"
/db_xref="UniProt/T/EMBL:Q9M3W4"
translation="DEPNTIGSNNTVRSKSNVLGNNDNTVSGDNNNSVSGSNNTV
VSGNDATVSGSNHVSSTNHIVTDNNNNVSGDNNVSGSFHTVSGGHTVSGSNNTVS
GSNHVSGSKNVDTDA"
mat_peptide
1..354
/product="ice recrystallisation inhibition protein"
/notes="ORF1"

```

ORIGIN

```

Query Match 27.0%; Score 264.2; DB 8; Length 357;
Best Local Similarity 83.8%; Pred. No. 2.4e-60;
Matches 299; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 482 GATGAAGAACCAATACAAATATCAGGACCAACAAATAGTGTGGATCAGGAGCAACAAT 541
DB 1 GATGAACAGCGGAATACGATTCTCGGAGCAACAATATCTGTGATCGGAGCAAAAAT 60
QY 542 GTTGTTCGGGAATGACAAACCGTCTGATCTGGGAAATACCAACCATGTGTCTGGAGC 601
DB 61 GTTCTTGTCTGGGAATGACAAACCGTCTATCTCGGGACAAACAATAGTGTCTGGAGC 120
QY 602 AACACACTGTGTAACCTGGAAGTGAACAATCTGTAGTGTGTAACCAACCATGTGTGATCA 661
DB 121 AACACACTGTGTAAGTGGGAATGACAAATACCGTAACCGGAGCAACCATGTGTGATCA 180
QY 662 GGGCAAAAGCATATTTGTTACTGATAACAATATGTTGATCTCGGGAACGCAATAATGTG 721
DB 181 GGGCAAAACCATATCGTTTACAGACAAACAATAACGATCTCGGGAACGATAAATGTA 240
QY 722 TCTGGAAGTCTTCATCTGTAACGAGGAGCAACAATACCGTATCTCGGAGCAACAATACT 781
DB 241 TCCGGAGCTTTTCATACCGTATCTCGGGGGGACAAATCTGTCTCGGAGCAACAATACC 300

```

305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, URL: <http://cdna01.dna.affrc.go.jp/cdna/>)
 This clone is one of the 32K full-length cDNA clones from japonica rice.
 NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Yamamoto, M. and Nakahama, Y.
 PAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, K., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carrinci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
 Location/Qualifiers
 1. .3392
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="J033108010"

ORIGIN

Query Match	8.1%;	Score 79.4;	DB 8;	Length 3392;
Best Local Similarity	63.1%;	Pred. No. 4.4e-10;		
Matches 157;	Conservative	0;	Mismatches 86;	Indels 6; Gaps 2;

Qy 104 GCAACGTCGTGGTTCGTGCCACCACGACGACCTCCACGCGTTGAGGGCGCCTCGCTGAGAAC 163

Db 202 GCTCGCGGCGGCATGTCACCCGGAAGACCTCTCGCGTCGCGGCATTTGCGGGGAAT 261

Qy 164 CT---AAGCGGCAAGAGCGTCGCGCTCGCGCGCGCATGTCGCGGCGCTCATGTCGC 220

Db 262 CTCTCTCGCGGTGGGGCGCGCGCGACCTCGCGCGCGTGTGTCGGGTACACGCTGTCGC 321

Qy 221 AGCTGGGAGGTGTGGATGCGNAACAGCAGCGGCGCGTGTGTCGGGTGCGGCTCCCC 280

Db 322 GCCTGGGAGGCGTCGCCCTGCGACGCGC---CGCCGAGTACACGCGCTGCGCCTCCCC 378

Qy 281 AAGCGCGCGCTTGGAGGGGATCATCCCATCGTCGATTGTCAGCTTGATCACCTTCGCTAT 340

Db 379 GGGCGAGGTCTGAGGGGGCCATCCCGCCTCCTCGCGCCTCGCGGCTCCAGGAC 438

Qy 341 TTGGATCTC 349

Db 439 CTCGACCTC 447

RESULT 5
 AP004342
 LOCUS
 DEFINITION
 Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 7,
 PAC clone:P0585H11.
 AP004342
 ACCESSION
 VERSION
 AP004342.5 GI:50510014
 KEYWORDS


```
/db_xref="GI:23617051"
/translation="WAAMKQVSSGGRQLLSVYLVAAVVIILPATSSRRPQCIWRE
DRGVATHLHFDVLDGADATVDVNGTGRAFDVAGLFGQVVMDDVLTGEPSPR
SSPRVGRTOGVFVSDMNVPAALLFCNVVLTAGPVAGSTVTLGRDHTQPIRELSV
GCTGAPRMATGVYLNRTASQPRADAVLELDVHVTRPEYLSQPPPPHRRPPPTTV
VT"
15804..16324
/gene="P0585H11.107"
join(<15804..15851,16016..>16324)
/gene="P0585H11.107"
/notes="start and end point are not identified"
join(15804..15851,16016..16324)
/gene="P0585H11.107"
/notes="predicted by GENSCAN etc."
/codon_start=1
/product="hypothetical protein"
/protein_id="BAC20740.1"
/db_xref="GI:23617052"
/translation="MSRPVPTTTRASKIRREGRQDGGGEMARSWRRGGGGG
RRGGGKWRSSRAAATSPDPAGGEATAVEPPDPAATISFACGNDGGGLP
TGDGHPQPSRLVAA"
complement(20109..20613)
/gene="P0585H11.108"
complement(join(<20109..20350,20514..>20613))
/gene="P0585H11.108"
/notes="start and end point are not identified"
complement(join(20109..20350,20514..20613))
/gene="P0585H11.108"
/notes="predicted by FGENSEH etc."
/codon_start=1
/product="hypothetical protein"
/protein_id="BAC20741.1"
/db_xref="GI:23617053"
/translation="MSGCLILLMIIVISASSATMIIVISNSSSAAAGRRRM
EYGGGCGVSKTWNKRLCTKGTCTAGEDYGCYNRPSPFGRFFHVCYSM
NYCKNIIIPSS"
26261..29293
/gene="P0585H11.109"
<26261..>29293
/gene="P0585H11.109"
/notes="start and end point are not identified"
26261..29293
/gene="P0585H11.109"
/notes="contains EST(s): AU056601(S20723),AU056602(S20723)
contains full-length cDNA(s): AK064359"
/codon_start=1
/product="putative phytosulfokine receptor"
/protein_id="BAC20742.1"
Query Match      8.1%; Score 79.4; DB 8; Length 149371;
Best Local Similarity 63.1%; Pred. No. 8.9e-10;
Matches 157; Conservative 0; Mismatches 86; Indels 6; Gaps 2;

QY 104 GCAACGTGCTGTCGTCACACAGACAGACCTCCACGCTTGAAGGCGCTCGCTGAGAAC 163
DB 26336 GCTGCGCGCGCGCATGCCACCGGAGACCTCTCGCGCTCGCGGCAATTTGCGGGGAAT 26395
QY 164 CT---AAGCGGCAAGAGCGCTCGCGCTCGCGCGCATGTCGCGGCTCATCTGCTC 220
DB 26396 CTCTCTCGCGGTGGGCGCGCGCGGACCTCCGCGCGCGTGGTGGCGTGCCTGCTGC 26455
QY 221 AGCTGGAGAGTGTGGGATCGGAAACAGCAAGCGCGCGCTCGTGGCGTGGCGGCTCCCC 280
DB 26456 GCTTGGAGCGCGTCTCGCTCGAGCGCGC---CGCCGAGTACGCGGCTGCGCTCCCC 26512
QY 281 AAGCGCGGCTTGAAGGAGATCATCCATCGTCGATTTGGTGGTGTATCATCACTTCGCTAT 340
DB 26513 GGGCGAGGTCTCGAGGGGGCCATCCCGCCCTCTCGCGCCCTCGCGCGCTCCAGGAC 26572
QY 341 TTGATCTC 349
DB 26573 CTCGACCTC 26581
```

```
RESULT 6
CR382398/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
gene
CDS
```

```
CR382398 349418 bp DNA linear INV 30-MAR-2004
Plasmodium falciparum chromosome 6, complete sequence; segment 1/5.
CR382398 AL844505
CR382398.1 GI:46362238
HTG.
Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 349418)
Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D.,
Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K.,
Buckee, C.O., Burrows, C., Cherevach, I., Chillingworth, C.,
Chillingworth, T., Christodoulou, Z., Clark, L., Clark, R., Corton, C.,
Cronin, A., Davies, R., Davis, P., Dear, P., Dearden, F., Doggett, J.,
Feltwell, T., Goble, A., Goodhead, I., Gwilliam, R., Hamlin, N.,
Hance, Z., Harper, D., Hauser, H., Hornsby, T., Holtroyd, S.,
Horrocks, P., Humphray, S., Jagels, K., James, K.D., Johnson, D.,
Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Lark, N.,
Lawson, D., Lennard, N., Line, A., Maddison, M., McLean, J., Mooney, P.,
Moule, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A.,
Rabinowitz, E., Rajandream, M.A., Rutter, S., Rutherford, K.M.,
Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R.,
Squares, S., Stevens, K., Tivey, K., Tivey, A., Unwin, I.,
Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and
Barrell, B.G.
Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13
Nature 419 (6906), 527-531 (2002)
22255708
12368867
2 (bases 1 to 349418)
Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K.,
Berriman, M., Pain, A., Hall, N., Atkin, R., Chillingworth, C.,
Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M. and
Barrell, B.G.
Unpublished
3 (bases 1 to 349418)
Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K.,
Berriman, M., Pain, A., Hall, N., Atkin, R., Chillingworth, C.,
Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M. and
Barrell, B.G.
Direct Submission
Submitted (20-SEP-2002) P.falciparum Genome Sequencing Consortium,
The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA, UK
4 (bases 1 to 349418)
Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K.,
Berry, A.E., Berriman, M., RA Pain, A., Hall, N., Atkin, R.,
Chillingworth, C., Doggett, J., Ormond, D., Sanders, M., Hayes, R.,
Hall, S., Quail, M. and Barrell, B.G.
Direct Submission
Submitted (26-MAR-2004) P.falciparum Genome Sequencing Consortium,
The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA, UK
For more information about this sequence or the Malaria Project,
see http://www.sanger.ac.uk/projects/p\_falciparum.
Location/Qualifiers
1..349418
/organism="Plasmodium falciparum 3D7"
/mol_type="genomic DNA"
/isolate="3D7"
/db_xref="taxon:36329"
/chromosome="6"
complement(653..1432)
/gene="VAR pseudogene"
/locus_tag="PFF0005c"
/pseudo
complement(653..1432)
/gene="VAR pseudogene"
/locus_tag="PFF0005c"
/notes="MAL6P1.317"
```


QY 759 CCGTATCCGGAGCAACAATCGTATCGGAGGACCAACATATCGTATCTTGGGAGCAACA 818
 Db 273194 TGGTGGATGATAACAACAATATGTTGGATGATAACAACAATATGTTGGATGATAACAATA 273135

QY 819 AAGCTCGTAACAGATGGTTAA 838
 Db 273134 CTATGCGTAGCGAAGATGAA 273115

RESULT 7
 AK064359 2238 bp mRNA linear PLN 24-JUL-2003
 LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:002-108-B08, full
 DEFINITION insert sequence.
 ACCESSION AK064359
 VERSION AK064359.1 GI:32974377
 KEYWORDS FLI_CDNA; oligo-capping.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1
 AUTHORS The Rice Full-length cDNA Consortium, National Institute of
 Agrobiological Sciences Rice Full-length cDNA Project Team;
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
 Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
 Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
 Genome Sequencing & Analysis Group; Ohtsuki, Y., Tsunoda, Y.,
 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
 Kurotsaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Nariakawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
 Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
 Kusumegi, T., Oka, M., Ryu, K., Ueda, M., Matsuura, K., RIKEN;
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
 Hara, A., Hashizume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
 Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
 Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
 Yoshino, M., and Hayashizaki, Y.
 COLLECTION, mapping, and annotation of over 28,000 cDNA clones from
 Japonica rice
 JOURNAL Science 301 (5631), 376-379 (2003)
 MEDLINE 22752273
 PUBMED 12869764

2 (bases 1 to 2238)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
 Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,
 Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
 Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
 Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
 Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
 Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Kurotsaki, T., Kusumegi, T., Li, C., Lu, M.,
 Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
 Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,
 Namiki, T., Nariakawa, R., Niikura, J., Nishi, K., Nomura, K.,
 Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
 Osato, N., Ota, Y., Ootomo, E., Ryu, R., Saitoh, H., Sakai, C., Sakai, K.,
 Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
 Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
 Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
 Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
 Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
 Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
 Yoshimura, A.
 DIRECT SUBMISSION
 TITLE Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
 JOURNAL Agrobiological Sciences, Department of Molecular Genetics, Head of
 LABORATORY Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp)

Tel:81-29-838-7007, Fax:81-29-838-7007)
 This clone is one of the 28K full-length cDNA clones from japonica
 rice.
 URL : http://cdna01.dna.affrc.go.jp/cdna/
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
 Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
 Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
 Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and
 Yamamoto, M.
 FAIS Genome Sequencing & Analysis Group: Ohtsuki, Y., Iida, Y.,
 Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
 Kodama, T., Kurotsaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
 Mizuno, K., Nariakawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,
 Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
 Yoshimura, A., Matsubara, K. and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center
 and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
 Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
 Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
 Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
 Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,
 Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
 Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
 Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
 Yasunishi, A. and Hayashizaki, Y.
 Location/Qualifiers
 FEATURES
 source
 1. 2238
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="002-108-B08"
 ORIGIN
 Query Match 7.6%; Score 74.8; DB 8; Length 2238;
 Best Local Similarity 68.4%; Pred. No. 7 le-09;
 Matches 119; Conservative 0; Mismatches 52; Indels 3; Gaps 1;
 QY 291 TTGGAGGGATCATCCCATCGTCGATGGTGAGCTGATCACCTTCGCTATTGGATCTCT 350
 Db 172 TGGTTGGCACCATCCCTGAATGCGATCGGTCAACTTGATTAACCTGACCTACTTGGATCTTT 231
 QY 351 CGGTTAATTCATTTGGTTGGGAGGTACCAAAAGTTTGCAGATACGGCTCAAGAGCTCA 410
 Db 232 CAACAAATTTCTTAGTTCGGCGAGATACCGAAGAGTTT---GACGCGAGCTCAAGAGCTTG 288
 QY 411 CCACTGCACAGCGAGTCACCTCGGTATGGTTCATTAACATGCTATTGCATGCA 464
 Db 289 TCACGCCCGAGCTTCGCCGGTATGGCGTTACTTAACATGCGTTGTATGCA 342

RESULT 8
 AK03166 2958 bp mRNA linear PLN 24-JUL-2003
 LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:J033121B13, full
 DEFINITION insert sequence.
 ACCESSION AK03166
 VERSION AK03166.1 GI:32988375
 KEYWORDS FLI_CDNA; CAP trapper.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1
 AUTHORS The Rice Full-length cDNA Consortium, National Institute of
 Agrobiological Sciences Rice Full-length cDNA Project Team;
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,

Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Ootomo,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN,
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice

Science 301 (5631), 376-379 (2003)
22752273
12869764
2 (bases 1 to 2958)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayashizaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T.,
Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K.,
Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M.,
Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,
Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M.,
Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A.,
Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,
Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K.,
Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H.,
Osato,N., Ota,Y., Ootomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,
Shingawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S.,
Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y.,
Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
Yoshimura,A.
Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL : <http://cdna01.dna.affrc.go.jp/cdna/>
NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Ootomo,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kouda,M.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,

Yasunishi,A. and Hayashizaki,Y.
FEATURES
source
Location/Qualifiers
1..2958
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J033121E13"
ORIGIN
Query Match 7.6%; Score 74.8; DB 8; Length 2958;
Best Local Similarity 68.4%; Pred. No. 7.5e-09;
Matches 119; Conservative 0; Mismatches 52; Indels 3; Gaps 1;
Qy 291 TTGGAGGATCATCCCATCGTCGATGGTGGAGTTCGATCCTCGCTTATTTGATCTCT 350
Db 1025 TGGTTGGCACCATCCCTGAATGATCGTCACTTAACCTGACCTTACTTGGATCTTT 1084
Qy 351 CGGGTAATTCATTCTTGGGGAGGTACCAAAAGTTTGCAGATACGGCTCAAGAGCCTCA 410
Db 1085 CAACAATTCCTTAGTCGGCGAGATACCGAAGATT---GACGAGCTCAAGAGCCTTG 1141
Qy 411 CCACTGACAGCAGCTACTCGGTATGGGTTCCATTAACATGCTATTGTCATGTGA 464
Db 1142 TCACCGCCGACGTTGCGCGGTATGGGTTCACTTAACATGCGCTTGTATGTGA 1195
RESULT 9
CNS08CBF/c 176237 bp DNA linear PRI 19-SEP-2002
LOCUS Human chromosome 14 DNA sequence BAC R-731P5 of library RPCI-11
DEFINITION from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION AL928742
VERSION AL928742.3 GI:23306225
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 176237)
AUTHORS Heilig,R., Pettit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,
Gvavay,G., Saurin,W. and Weissbach,J.
TITLE Sequencing of the human chromosome 14
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 176237)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
On Sep 24, 2002 this sequence version replaced gi:23306222.
----- Genom Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: <http://www.genoscope.cns.fr/>
Contact: Secref@genoscope.cns.fr

The following sequence is oriented from the T7 to the SP6 end.
----- Finishing boundaries
FINISHED SEGMENT STARTS AT BASE 1
FINISHED SEGMENT ENDS AT BASE 124850
----- Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 11.37x in Q20 bases; sum-of-contigs

Overall quality chart :
Range : Bases
0 :
1 - 9 : 1


```

10 - 19 : 48
20 - 29 : 165
30 - 39 : 825
40 - 49 : 3919
50 - 59 : 6201
60 - 69 : 8574
70 - 79 : 22106
80 - 89 : 54448
90 - 99 : 79950
-----
Percentage of bases with a quality value >= 40 : 99 %.

FEATURES
source
  Location/Qualifiers
    1. .176237
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
      /chromosome="14"
      /clone="R-731F5"
      /clone_lib="RPCI-11"
      14470..14567
      /note="matching EMBL:G14654
      RHdb:RH7974
      dbSTS:STS21065
      Identified using the e-PCR software (G. Schuler)"
      57606..57752
      /note="matching EMBL:L00022
      RHdb:RH69981
      dbSTS:STS48887
      Identified using the e-PCR software (G. Schuler)"
      60040..60260
      /note="matching EMBL:M55420
      RHdb:RH80278
      dbSTS:STS56700
      Identified using the e-PCR software (G. Schuler)"
      69316..69421
      /note="matching EMBL:H26187
      RHdb:RH44850
      dbSTS:STS37918
      Identified using the e-PCR software (G. Schuler)"
      145938..146060
      /note="matching EMBL:Z53040
      RHdb:RH9751
      dbSTS:STS5550
      Identified using the e-PCR software (G. Schuler)"
      158529..158653
      /note="matching EMBL:AA160692
      RHdb:RH48485
      dbSTS:STS41544
      Identified using the e-PCR software (G. Schuler)"

ORIGIN
Query Match 7.2%; Score 70.2; DB 9; Length 176237;
Best Local Similarity 56.5%; Pred. No. 2.8e-07;
Matches 130; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 600 GCACCAACACTGTGTGAATCGGAAGTACAAATCTAGTTGGTAGCAACCATGTCGTAT 659
DB 7784 GAAGCATCCAGATCGGNACAGGAATGTCAGCATGGACAGGAAGCATCCAGAATGTAA 7725
QY 660 CAGGGACAAAGCATATGTTTCTGATAACAATAATGTTGATCCGGGAACGACAATAATG 719
DB 7724 CAGGAAGCATCCAGATCGGAACAGGAATGTCAGCATGGACAGGAAGCATCAAGATG 7665
QY 720 TGTCTGGAGTTCATCATCTAGTATCAGGGAGCACATACCGTATCCGGGAGCAACATA 779
DB 7664 TAACAGGAAGCATCCAGATGGGAACAGGAATGTCAGCATGGACAGGAAGCATCCAGA 7605
QY 780 CTGTATCCGGGAGCAACATATCTGTATCTGGGAGCAACAAAGTCGTAACA 829
DB 7604 ATGTAACAGGAAGCATCCAGATGGACAGGAAGCATCCAGATGGACAA 7555

RESULT 10

```

```

CNS01DT2 169802 bp DNA linear PRI 19-NOV-2001
LOCUS Human chromosome 14 DNA sequence BAC R-417P24 of library RPCI-11
DEFINITION from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION AL122127
VERSION AL122127.6 GI:17026193
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS 1 (bases 1 to 169802)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,
Gyapay,G., Saurin,W. and Weissbach,J.
Sequencing of the human chromosome 14
Unpublished
2 (bases 1 to 169802)
Genoscope.
Direct Submission
Submitted (19-NOV-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Nov 20, 2001 this sequence version replaced gi:14715169.
-----
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
-----
The following BAC sequence is oriented from the T7 to the SP6 end.
-----
Assembly program: Phrap; version 2.0
Quality coverage: 7.56x in Q20 bases; sum-of-contigs
-----
Overall quality chart :
Range : bases
0 :
1 - 9 :
10 - 19 :
20 - 29 : 11
30 - 39 : 159
40 - 49 : 4325
50 - 59 : 11964
60 - 69 : 13264
70 - 79 : 28113
80 - 89 : 55713
90 - 99 : 56253
-----
Percentage of bases with a quality value >= 40 : 99 %.

FEATURES
source
  Location/Qualifiers
    1. .169802
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
      /chromosome="14"
      /clone="R-417P24"
      /clone_lib="RPCI-11"
      11427..11641
      /note="matching EMBL:G33053
      RHdb:RH67749
      dbSTS:STS47676
      Identified using the e-PCR software (G. Schuler)"
      11439..11536
      /note="matching EMBL:G14654
      RHdb:RH7974
      dbSTS:STS21065
      Identified using the e-PCR software (G. Schuler)"
      39191..39405
      /note="matching EMBL:G33053
      RHdb:RH67749

```

	dbSTS:STS47676	
STS	Identified using the e-PCR software (G. Schuler)"	
	39203..39300	
	/notes="matching EMBL:G14654	
	RHdb:RH7974	
	dbSTS:STS21065	
STS	Identified using the e-PCR software (G. Schuler)"	
	39281..39447	
	/notes="matching EMBL:X99549	
	RHdb:RH71306	
	dbSTS:STS51071	
STS	Identified using the e-PCR software (G. Schuler)"	
	131895..132128	
	/notes="matching EMBL:X00253	
	RHdb:RH18069	
	dbSTS:STS3713	
STS	Identified using the e-PCR software (G. Schuler)"	
	147503..147627	
	/notes="matching EMBL:R05773	
	RHdb:RH53956	
	dbSTS:STS23199	
ORIGIN	Identified using the e-PCR software (G. Schuler)"	
	Query Match 6.9%; Score 67.2; DB 9; Length 169802;	
	Best Local Similarity 55.6%; Pred. No. 1.8e-06;	
	Matches 129; Conservative 0; Mismatches 103; Indels 0; Gaps 0;	
Qy	599 AGCAACAACTCTTTGAATCGAAGTGCACAATACTGTATTGGTAGCAACCATGTCGTA 658	
Dd	19413 AGAAATCATCAACATGGAACAGGAAGCATCCAGAATGGAAGGAAGCATCCAGCATGGA 19472	
Qy	659 TCAGGACAAAGCATATTGTTACTGATACAAATAATGTTGTATCCGGNACGCAATAAT 718	
Dd	19473 ACAGGAAGCATGCAGAGTGGAACAGGAACAGTCCACATGGAACAGGAAGCATCCAGAGT 19532	
Qy	719 GTGCTCTGGAAGCTTCCATATCTGTATCAGGGGACCAATPACCGTATCCGGAGCAACAAT 778	
Dd	19533 GGAACAGGAAGCATGCAGAGTGGAACAGGAATGTTCCAGCATGGAACAGGAAGCATCCAG 19592	
Qy	779 ACTGTATCCGGAGCAACCATATCTGTATCTGGAGCAACAAGTCGTAAACAG 830	
Dd	19593 CATGGAACAGGAAGCATGCAGATGGAACAGGAGCATCCAGATGGAACAG 19644	
RESULT 11		
AF372178		
LOCUS	646 bp DNA linear PLN 18-JUN-2002	
DEFINITION	Leptocoryphium lanatum DNA-directed RNA polymerase beta, subunit 2 (rpoC2) gene, partial cds; chloroplast gene for chloroplast product.	
ACCESSION	AF372178	
VERSION	AF372178.1 GI:16551242	
KEYWORDS		
SOURCE	chloroplast Leptocoryphium lanatum	
ORGANISM	Leptocoryphium lanatum	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Paniceae; Leptocoryphium.	
AUTHORS	1 (bases 1 to 646)	
TITLE	Duvall,M.R., Noll,J.D. and Minn,A.H.	
JOURNAL	Phylogenetics of Paniceae (Poaceae)	
REFERENCE	Am. J. Bot. 88 (11), 1988-1992 (2001)	
AUTHORS	2 (bases 1 to 646)	
TITLE	Duvall,M.R., Noll,J.D. and Minn,A.H.	
JOURNAL	Direct Submission	
FEATURES	Submitted (18-APR-2001) Biological Sciences, Northern Illinois University, Montgomery Hall, DeKalb, IL 60115, USA	
source	Location/Qualifiers	
	1..646	
	/organism="Leptocoryphium lanatum"	
	/organelle="plastid;chloroplast"	
	/mol type="genomic DNA"	

TITLE Direct Submission
 JOURNAL Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
 COMMENT On Oct 3, 2002 this sequence version replaced gi:5731897.
 For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
 FEATURES
 source 1..347582
 /organism="Plasmodium falciparum 3D7"
 /mol_type="genomic DNA"
 /isolate="3D7"
 /db_xref="taxon:36329"
 /chromosome="4"
 /clone="NAL4P1"
 10384..32958
 /notes="rep20 Repeats"
 join(35153..41725,42757..44124)
 /genes="VAR"
 /notes="synonym: PFD0005w"
 join(35153..41725,42757..44124)
 /genes="VAR"
 /notes="Similar to Plasmodium falciparum variant-specific surface protein var-2 SWALL:Q26033 (EMBL:L40609) (2664 aa) fasta scores: E(): 7.8e-149, 43.1% id in 2872 aa"
 /codon_start=1
 /product="erythrocyte membrane protein 1 (PfEMP1)"
 /protein_id="CAD49094.1"
 /db_xref="GI:23498127"
 /db_xref="GOA:Q81220"
 /db_xref="UniProt/TrEMBL:Q81220"
 /translation="MYRTGSGGGVDKDGIDHQSAHLLDSIGKVKHQVKNAGDGT GAGSDAKNYIDDLGDLQAPINPKLIGTDDPCPLRVLYNNVNGDGGKRGYPCTE LSGKQFPSPDITGGQCTNSKMRSCGACAPYRLHLCHNLRSIETTSKASDTL LLEVCNAAKVEGSSINHYTKHSHKSDSPSLCTVLARSFADIGLVRGKDLFYGT YESAREKLENNKGVFGKIHGSLSEAKKYQDGGNTYQLREDDWTANRETFTVKAI TCEVNGNIFRATCGDEKKNPSLTSKCRDKDAGKPIKSGNVNIVPTFYDYVQY LRWFWEADFCRLRHKLKDAIKKCRGNKEBYCDLNRDCKNTASGKHFFEDFD CKDQVSCAFPDMWIDONKLEPLKQKVTYKETSQSGCGSKRKRDAATTNYEYE KFYELKGTGYKVVANFLEKLNDEVDCTKNNDIKDGNIDPKNVHSGSAKGDGNVK TYRTYCBACPCWGAKEGVGKAEKSCQTKDYPDKTTIILTGDTKRSQVCL KYKFGNGNGSGKATNATREKGGDKQKWKICYDENKKYGSDAINFVCL QDQKRGKQVTSYNAPFWKVMHLDHVSVERLNSCINNASKQCNKNECKNE CGCFKRWQKKEWEAKIDHFGKQKDIIEOTGCDAGTVLAALKLEFLNEDTEKS EKLDAEAEKIKHLQMLEOAGVRDLAAVGGPCTEGVABQNTIMDKFLDLSEKAE QCKNCPKAAQSGSPGARSADSPAGTREDHPDAEDDDDDDDDDDEDESEEREED PQCKTVNDILSTDRTQVGDCHERYKNGPWPWCGDLTLDVDTKVCMPRRQKLCI YIIAHSEYKNIETQDRLDAFIRTAATAETFLSQYIKIKNADAKQLDNGTIPPEFL RSMYFTGYDRDICTLNTDISKTVNDVAKADIKGFPKSGSPSGTTPQDWQTY GKDIWKGIMCALHTVNTTEKTKIKNDYSYKVNQSGNPSLEDPAKKPFLRWMI EWEEFCBAERGLQENIGKSCNGINPIQYCDNRHPCNACDEYKNYVETKQEPGQ TTKFVRDANLENADQRYKDYKTQGPSKOGNDYLDKDCNKKCSMEGNVLTDSVSK PFGIIAHKYSKCNCLGAKFVTPNPPAPPPPPPPAIPAPATPTGVNPELWTLF SUTNKPACTLKYGKAPTSWKCIPTGNTSNEGADVSDSGDAKRHRDRDLAPSSG NQSGICVPPRRRLKYTLTKWABETTKGSKGSEAGETSESSSEASSPGETSSQ GSKSPGLSTPASTSPSSRDDLLKAFVESAETFFLHWKYMOKDEKDEKKQ ORESGLVGLADNGSVNDDKDPQKLEKGDIPPEFKQPMFTLADGIDILVRGQNT SDSEGTGNSNNNIIVLEAGDKODEMKIKQADEHINSIKQAASVNPORPQOQN SSLITRETLKEHAPSWEGMICALTYKENDKKLVKDNVEYKFTGTTTSGTKYKE KLEYNTVKLDENSDDTAKOTATAPSDNTPTFLSHVPAFLKPCGREGCRKYTKERK KKLQAQKVCDDADSAKYCSGEECKIEDISINHFVADLKPCGREGCRKYTKERK KTIPEFQSEYFHTHKDCPCSFKIDCRNGKSKGDTKGGCDGTTTIDAKEIAKMTSS TPDVNRVSDNNTTEGGDLKVCBKGIFKGIKBEKCRNECGDLVCGLKGDNGG KLDQDKIILRALIKWLEFYLDYINKIKHKISDCINNGEKNICRDKCNKCNCGEW IKUKGEWEKIKRHLKLEKNGDMMKSVNRFLEKPEHFPNFKAIKFCGLTPES FCGLNGDKSQNGHQAIDCMIKKJEDKITSCLSTSGEQTETCEQHTPLPDEDLL LEETENVGKQSGFCPCVBEKETEYDEGKEDTSEPTKEDTEESKKKSDPSLP EPPATPEAPEEKKEVPOPOPTTPOIVDTPALVTSTLAWSGVIGFAAFTYFPL KTKYKTDILLRLVINPKSDYDIPTKLSPNRYIPYTSKRYGRKRYIIVLGGSDTSGY THYSDITSSSESEBEMDINOIYAPRAPKYLTLIEVLEPSSNNTAGNNTASGN NTASGNNTASGNTPSDQNDIQSDGIPSSKITDNWNTLKDEFISQYIQSEQPKD VPNDYSSGDIIPFNTQHTLYFDKPEDEKPFITTSIHDRNLTYGEEYNIDMSTNSGNDLY

NGKNLDYSGNNVYSGIDTSDNRGLTSGKHSYSGIDLINDTLNQHIDYDEVLK
 RKESEFGNTHVHTTINRPAKPARDDPDLNQLLEFHTLWDRHRNCEKNNKBELLD
 KKEWENETSGNTHSDSNKLTADVSIQIDMDNPKPINQFNTNDINVTPTMDNM
 EDDIYVDVNDHDTSTVDSNTMDVPVKQIEMDVNTKLVKEKYPIADVMDI"
 45458..46601
 /gene="PFD0010w"
 /gene="PFD0010w"
 /gene="PFD0010w"
 /note="VAR exon II, could be alternate exon II for
 upstream VAR gene PFD0005w"
 complement(join(48479..49537,49768..49821))
 /gene="RIF"
 /note="synonym: PFD0015c"
 complement(join(48479..49537,49768..49821))
 /gene="RIF"
 /note="1 probable transmembrane helix predicted by
 TMHMM2.0 at aa 328-350
 Similar to Plasmodium falciparum rifin pfb0030C
 SWALL:O96112 (EMBL:AE001367) (370 aa) fasta scores: E():
 3.4e-65, 53.6% id in 375 aa"
 /codon_start=1
 /product="RIFIN"
 /protein_id="CAD49095.1"
 /db_xref="GI:23498128"
 /db_xref="UniProt/TrEMBL:Q81219"
 /translation="MKIHYINILLFELPLNLIYNNQHNKSTNLHTNNRSLCECELY
 APATYDDDPQMEKVMVYFSKQQRFEYDERMVKRQCKDKCKEIKQIILDKME
 LMDKFAFATLOIADPTVCSEKSLADKVGCGYGLGTVAFTVGLTGSVAV
 HWKPKALEAAIAKAIAGTADIAAEEAAGKARGMEFVIKALKHFGVGNFPFGICDT
 ISSTGNTYKTFEVTIYSKYNGTCNLMRSSINPTACYITIELSKITGAGTGDRPP
 LVAIRMIKGLAEATEAAKAAAKNAKLTAKREKOTALIEAGFNSSITSINASTII
 AILIVIMIIYIILYRRKKMKKKLQYIKLKE"
 complement(join(52002..53297,54200..63307))
 /gene="VAR"
 /note="synonym: PFD0020c"
 complement(join(52002..53297,54200..63307))
 /gene="VAR"
 /note="Similar to Plasmodium falciparum variant-specific
 surface protein var-3 SWALL:Q26032 (EMBL:L40609) (3006 aa)
 fasta scores: E(): 6.2e-103, 43.31% id in 3551 aa"
 /codon_start=1
 /product="erythrocyte membrane protein 1 (PfEMP1)"
 /protein_id="CAD49096.1"
 /db_xref="GI:23498129"
 /db_xref="GOA:Q81218"
 /db_xref="UniProt/TrEMBL:Q81218"
 /translation="MGTGSSSTPSVKDVNESHNSARNVLENIIGIYNEEKKKVNGY
 TSQKGLDLSRAPHDGLRKAALGVIPGPANSCDLDMKFTNTINNGYPPARNPDDLNR
 QNRGENAAYCNSDKIRVTGKKSAGGACAPFRQRQMDKNLEYLNTDNTDDTLIG
 NYLVATKYGESIVAKHPHENSEVCTALARSFADIGTIVRGKMFKNREEDAVQKGL
 RAVFKINDNLEKEISDYNDPNYKREDWNTANRDQVWRAITCYIPYVNYFKKT
 SDDTIVTNDGKGVHGPATNLDVYPOFLRFDWAEFCRIRHKLKIKDACRN
 DEXLYCSQNGYDCTKRIEKSGSREKNTGCSNKKVDYDFWELQOQNEFKIQDKY
 DKEIETVNTKPISNSNTKKEYIKFEELKKGYSVNFLLQNLNGRYCOEKIIE
 EDIAFTKQNHAFYRSDYQCPDPCVVECDGKTQKTDNDDNCRSKIKILISE
 TEIETVLYSDDKQGVITEKDKFCRGNPNYNDENLQKWKYCNKSNKNCIIMLY
 OPIKYNMELSECFHSAWKLNDITIRWEHOLKNCINNTNTVDTSKCIKNGCEVEA
 WTERKKDWEKLEKVLNKKDTSHTNYNKLKQVDFRFLQVFMALQDEKQWQFTE
 DLAKKPGSVESAGTANSQDAIEFLDLHLKDNALTCRDANSIKPCTYPPNPTNPGCT
 NNGGKLVKRLAEWMMQRRAKQLEKRGGEINLKADASQGYIRGGKELKNGQICN
 IDTSGVSNRNGNGGCTGKNDKRPKIGTEWSYGEHEKRRTHPEVMPRRHMCIS
 NLEKLDVSVIKGNASHLLGLDLAAKYEAKNIKELYQNNNSKNGVLDQNDKGTIC
 RAMKYSFADIGDIIRGKMVQNTATKLOAYLAKIFDKIKONKDIKGLQVNGDID
 HKLLREDWEANRHOVWRAMKCAIENDKMKNGIPIEDYIPORLAWMTWASWYCKE
 QRLGVELLEKQSCGKQCTEGVDCCKCAACDKYKDEINKWEQWTIKGKYKT
 LYKATKPGVTSNNPDKEDVDFLQKLPKRSKNTPGVTAMPTNLTYSAAQYIHQ
 ELGKTVGNTQKEDCNKKGKFAFHPKPEYEACICTQKQAQKPIEKDNCNGIKT
 LLDNSNGGTGIDGNGPKPIGNTYPSWNCENESKAENKACVPPRRKFCVSLKAGEI
 FKNKGEDIRETFVKSAALETYPAMKRYNDNKAEBELSGTIPENFKRQMYTFADY
 RUIFGTDITSDHLLDVSNAKMLKKNQKSVIIDDEKLADMMWKEHGHETWE
 GMLCAUTHIDEERKNIKSTYSYDQKKTKTGTTPLEKPAERQFLRWFTESWDFEC
 RERKKEBVEYKDKKEADHGCKNPKTGNHGVCSACKYEEYISTKKKQNTQKQKFD
 IDNKNGEENYKDKKEADHYLDKCFPGCTCYMEKVKNNSEYWDKPNKTYTNSDLEK

KCECKPOPPPPAPQOSACEI VDD ILNGSKSATDYTEKNGKYYGYRYPWNNCSOIH
RTHNGACMPRRQKQVFNTOYFKGTYDVLDFRATFKCAAEVTFLLHKYKSDJDNNGE
DLQNLSEIIPDFKRFQMYTFGTYDVFDFGTD I SKGSHIGSELAKEKIDYKFNNGE
KNPDLSCRDKNWNNNGPY I WKMGLSKKEKAWGKOT I KNSYNNHNHYKVS DNRNGDPL
ETAKRQFQRLWTFEMGDEPBRQKQOLD I KKKCPKEITNEGKKSCSKCAKAYE
WLOTWKEHYEQK I KYENDKSDYNDPTDQTSQPOAYLYNKKLEK I CPSGNTSANCEY
CKMY PSSQNNNNWPNASLDPTSDYKDTCEQKASRNFVSRSDEGDDGPPPPRPP
QRLARSANDPSPRPAPGPGPSTGPDAGARASTGSPPOQPXPAGNGGPPARIL
OPTARVDDEEDDEEDDESGSEGEDVDSDSDSEDEDEDEDDESHVDGHH
QESEPDPDETVBETVAAPBPACAEI VKELPDNTFKDQACNLKGVGNSRLGWKKI
PSGDT I VTSVNGDRSQRHRAAGEATGKSDSGSI I CVPRRVELVUGKLTOWASQRT
QSGTSSOIVKSSASQNSHPT I LPSNPNRDDGLRDARFASAAVEVTFFLMDR I KCLNTK
KPAATLGLLQ I PLAMGAINGVYPSGDNNQDQKLKEGEI I PEEFKRQMYDLYVDR I
LFGKND I VINTGSGADKEMKAKBEKI EKT I DKVPNNVSLVPTPTTAPKSDKRRKT
WFEANGHI I WKGM I YALT YDKNDEK I KYDNEVYKMLDEANKPKATKYQVKNVLE
ENGSAKTPQPSGSDGNT I PTL I SRPY I PLBEGWET I CRERKRELSVREKCR
GEYGEKY CGSDGDGTENGELATHNKPADLDCDCKQCRKYRW I D I KPEYEQK
DKYQGLDLKLGNSGNNNCKE I KHTSASEFLKELCKKQDQSDNTDKSDEKQ
NNKLDNFKPLTFNPT I CTPSPNKNVNGSGRGTRGDCPTPHNEKSGSVFVFN
NGNSGTE I VEMI I DREPL I KNTSK I BESSGNSDLSFTSLRSKVRQDQWECBYNA
EKTD I CKLNFNDK I DNLQNT I TFFVLEYLWQD I IGGY I LKRRKI I EOCKENGCTC
NENSKDNCAGKVAOKATWENO I KDHNYKRYGNGYDMSHKVNYFENENFETKWK
NENSKDNCAGKVAOKATWENO I KDHNYKRYGNGYDMSHKVNYFENENFETKWK

Query Match	6.5%;	Score 63.8;	DB 3;	Length 347582;
Best Local Similarity	50.5%;	Prod. No. 1.8e-05;		
Matches 155;	Conservative	0;	Mismatches 152;	Indels 0;
Gaps	0;			
540	ATGTGTGTTCCGGGAATGACACACGGTCGTATCTGGGNATAAACAACNATGTCCTGGGA	599		
233523	ATTATATATTATGATGAATGATTCTTTGTTGTAATATTATTTGTTTTTATAATATTGTCAGG	233582		
600	GCAACAACTGTTGTAACCTGGAAGTGACAACTACTGTAGTTGGTAGCAACCATGTCGTAT	659		
233583	GTTATTACAAATATTGTTTCATGGTTATTATATTATTTGTCAGGGTTATTACATATTGTC	233642		
660	CAGGGAACAAGCATATTGTTACTGTATACAAATAATGTTGTATCCGGGAACGCAATAATG	719		
233643	AGGGTTATTACAAATATTGTTTCAGGGTTATTACAAATATTGTTTCAGGGTTATTACAATATTG	233702		
720	TGTCGTGGAAGTTCATACTGTATCAGGGGAGCAAAATACCGTATCCGGGAGCAACAATA	779		
233703	TTCATGGTTATTATAAATATTGTTTCAGGGTTATTACAAATATTGTTTCACGGTTATTACAATA	233762		
780	CTGTATCCGGGAGCAACCATATCTGATCTGGGAGCAACAAGTCGTAAACAGATGGTTAAT	839		
233763	TTGTTTCAGGGTTATTACAAATATTGTTTCAGGGTTATTACAAATATTGTTTCAGGGTTATTACA	233822		
840	ATTCTGT	846		
233823	ATAATTGT	233829		

RESULT 13	
CQ741677	
LOCUS	300 bp DNA linear PAT 03-FEB-2004
DEFINITION	Sequence 27611 from Patent WO02068579.
ACCESSION	CQ741677
VERSION	CQ741677.1 GI:42350302
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL	Patent: WO 02068579-A 27611 06-SEP-2002;
FEATURES	PE Corporation (NY) (US)
source	Location/Qualifiers
	1..300
	/organism="Homo sapiens"

```

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match          6.4%; Score 62.8; DB 6; Length 300;
Best Local Similarity 55.5%; Pred. No. 8.7e-06;
Matches 121; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

Qy      613  TGTAACTGGGAAGTGACAATAACTCTGTAGTTGGTAGCAACCATGTCTGTATCAGGCACAAAGCA 672
Db      2    TGGGACAGGAAGCATCCAGATGGAAGAAGAGCATCCAGCATGGAACAGGAAGCATGCA 61
Qy      673  TATTGTTACTGTATAACAATAATGTTGATCCGGGAACGACAATAATGTGTGGAAGCTT 732
Db      62   GAGTGGAAACAGGAAACCGTCCACCATGGAACAGGAAGCATCCAGAGTGGAAACAGGAAGCAT 121
Qy      733  CCATACCTGTATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAG 792
Db      122  GCAGAGTGGAAACAGGAAATGTCAGCATGGAACAGGAAGCATCCAGCATGGAACAGGAAG 181
Qy      793  CAACCATATTCGTATCTGGGAGCAACAAGTCGTAACAG 830
Db      182  CATCCAGCATGGACAGGAGGATCCAGAGTGGAAACAG 219

RESULT 14
AC126139/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
Rattus norvegicus (Norway rat)
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
unordered pieces.
Rattus norvegicus clone CH230-104014, WORKING DRAFT SEQUENCE, 7
261587 bp DNA linear HTG 10-MAY-2003
AC126139

```

REFERENCE
AUTHORS

Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, J., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R.A., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 261587)
Worley, K.C.

Direct Submission
Submitted (04-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 261587)

Rat Genome Sequencing Consortium.
Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:24819414. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GHUO

Center clone name: CH230-104014

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 245312 bases at least Q40

Consensus quality: 249138 bases at least Q30

Consensus quality: 252151 bases at least Q20

Estimated insert size: 257796; sum-of-contigs estimation

Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 250010: contig of 250010 bp in length
* 250011 250110: gap of unknown length
* 250111 253467: contig of 3357 bp in length
* 253468 253567: gap of unknown length

* 253568 255148: contig of 1581 bp in length
* 255149 255248: gap of unknown length
* 255249 256807: contig of 1559 bp in length
* 256808 256907: gap of unknown length
* 256908 258585: contig of 1678 bp in length
* 258586 258895: gap of unknown length
* 258896 260166: contig of 1481 bp in length
* 260167 261587: contig of 1321 bp in length.
* 260267 Location/Qualifiers

FEATURES

source

1..261587
/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-104014"

misc_feature

1..2511

/note="wgs end_extension"

clone_end:T7"

misc_feature

2562..3793

/note="wgs end_extension"

clone_end:T7"

misc_feature

6414..7318

/note="clone_boundary"

clone_end:T7"

misc_feature

site:ECORI

end_sequence:BH325436"

complement(246622..247488)

/note="clone_boundary"

clone_end:Sp6

site:ECORI

end_sequence:BH325437"

ORIGIN

Query Match 6.2%; Score 60.8; DB 2; Length 261587;
Best Local Similarity 51.9%; Pred. No. 0.00011;
Matches 165; Conservative 0; Mismatches 147; Indels 6; Gaps 1;
QY 512 AACAAATAGTGTGGATCAGGAGCAACAATGTTGTTCCGGGAATGACACACGGTCGTA 571
Db 83753 ATCAGCACTGTTGTAGCATGTATCAGCACTGTTGTAGCATGTATCAGCACTTTTGTAGCA 83694
QY 572 TCTGGGAATACAAACCATGTGTCTGGGAGCAACAACACTGTTGTAACCTGGAAGTGAACAT 631
Db 83693 T-----GTATCAGCACTGTGTTAAACATGTATCAGCACTGTTGTAGCATGTATCAGCACT 83640
QY 632 ACTGTAGTTGTAGCAACCATGTGCTATCAGGAGCAACAACATATCTTACTGATAACAAT 691
Db 83639 GTTGTAGCATGTATCAGCACTGTTGTAGCATGTATCAGCACTGTGTTAATATGTATCAGC 83580
QY 692 AATGTTGTATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATACTGTATCAGGGGAG 751
Db 83579 ACTGTTGTAGCATGTATCAGCACTGTTTAAACATGTATCAGCACTGTTGTAGCATGTATC 83520
QY 752 CACAAATACCGTATCCGGGAGCAACAATCTGTATCCGGGAGCAACCATATCTGATCTGGG 811
Db 83519 AGCACTTTTGTAGCATGTATCAGCACTGTTGTAGCATGTATCAGCACTGTTGTAAACATGT 83460
QY 812 AGCAACAAAGTCGTAACA 829
Db 83459 ATCAGCACTGTTGTATACA 83442

RESULT 15

AC119701/c

LOCUS

DEFINITION

AC119701

VERSION

KEYWORDS

SOURCE

ORGANISM

AC119701 172927 bp DNA linear HTG 20-NOV-2002
Rattus norvegicus clone CH230-462N7, WORKING DRAFT SEQUENCE.

AC119701

HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;


```
Db 172320 AGCATGTATCAGCACTGGGGTAGCATGTATCAGCACTGTTGTAGCATGTATCAGCACTTT 172261
Qy 760 CGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAA 819
Db 172260 TGTAGCATGTATCAGCACTGTTGTAGCATGTATCAGCACTGTTGTAACATGTATCAGCAT 172201
Qy 820 AGTCGTAACA 829
Db 172200 TGGTATAACA 172191
```

Search completed: May 11, 2005, 02:51:19
Job time : 4640 secs

This Page Blank (uspto)